

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 106579

TO: James Schultz

Location: cm1/12e18/11e12

Art Unit: 1635

Wednesday, October 29, 2003

Case Serial Number: 09331204

From: Toby Port

Location: Biotech-Chem Library

CM1-6A04

Phone: 308-3534

toby.port@uspto.gov

Search Notes

Dear Examiner Schultz,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port





STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

Voluntary Results Feedback Form
> I am an examiner in Workgroup: Example: 1610
> Relevant prior art found, search results used as follows:
☐ 102 rejection
☐ 103 rejection
☐ Cited as being of interest.
Helped examiner better understand the invention.
Helped examiner better understand the state of the art in their technology.
Types of relevant prior art found:
Foreign Patent(s)
Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
> Relevant prior art not found:
Results verified the lack of relevant prior art (helped determine patentability).
Results were not useful in determining patentability or understanding the invention.
Comments:

Diopoli or send completed forms to STCB otech: Chem Library GMI = Cha. Desk



STIC-Biotech/ChemLib

106579

From:

Schultz, James

Sent:

Thursday, October 23, 2003 9:39 AM

To: Subject:

STIC-Biotech/ChemLib Seq Search request 09/331,204

Hello,

Could you please perform a length limited nucleotide sequence search against SEQ ID NOS: 4-8 and 13 in the above entitled application, where the maximum size of the returned hit is no longer than 22 nucleotides? SEQ ID NOS: 4, 5, 7, and 8 are 18mers, SEQ ID NO: 6 is a 21mer, and SEQ ID NO: 13 is a 12mer. This application recited multiple sequences as originally filed, before we started restricting to one sequence. Also, I need the <u>interference databases</u> searched.

Thanks, Doug Schultz

J. Douglas Schultz, Ph.D. AU 1635 (Biotechnology) Patent Examiner United States Patent and Trademark Office (703) 308-9355 (703) 746-3973 (fax) Office: CM1 12E18 Mail: CM1 11E12

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (wi	here applic.)
STN:	
DIALOG:	
Questel/Orbit:	·
DRLink:	
Lexis/Nexis:	_
Sequence Sys.:	`
WWW/Internet:	
Other (specify):_	

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Query Match 80.0%; Score 14.4; DB 1; Length 19; Best Local Similarity 93.8%; Pred. No. 1e+04; Matches 15; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 93.8
Matches 15, Conservative
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CORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
PCT-US02-38216-38943
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

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7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*

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          GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
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PCT-US02-38216-27376
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Sequence 41647, Application PC/TUS0238216

GENERAL INFORMATION:
APPLICANT: ROSELTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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PCT-US02-38216-38943
; Sequence 38943, Application PC/TUS0238216
; GENERAL INFORMATION;
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: GENES AND USES THEREOF
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT PLING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 38943
; LENGTH: 19
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PCT-US02-38216-51896
PCT-US02-38216-86378
PCT-US02-38216-68852
US-10-669-841-4725
US-10-669-841-4726
US-10-669-841-5015
US-10-669-841-5015
PCT-US02-38216-9770
PCT-US02-38216-9770
PCT-US02-38216-9731
PCT-US02-38216-9655
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PCT-US02-38216-9675
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PCT-US02-38216-9677
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Gaps

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Sequence 27376, Application PC/TUS0238216
GENBEL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
SOFTWARE: Patentin version 3.2
SEQ ID NO 27376
LENGTH: 18
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT PILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 27360
LENGTH: 19
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    GENERAL INFORMATION:
    APPLICANT: Rosetta Genomics LTD
    TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
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Pred. No. 1.4e+04;
0; Mismatches 0; Indels
                                                                                             Query Match 80.0%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 9.9e+03;
Matches 15; Conservative 0; Mismatches 1;
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; Sequence 27360, Application PC/TUS0238216
; GENERAL INFORMATION:
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PCT-US02-38216-27360
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-42141
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Matches 14; Conserv
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FCT-US02-38216-42141

Sequence 42141, Application PC/TUS0238216

GENERAL INFORMATION:

APPLICANT: Rosetta Genomics LTD

TITLE OF INVENTION: GENES AND USES THEREOF

FILE OF INVENTION: GENES AND USES THEREOF

FILE REFERENCE: 55002

CURRENT APPLICATION NUMBER: PCT/US02/38216

CURRENT FILING DATE: 2002-11-12

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: Patentin version 3.2

LENGTH: 22
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICATIS ROSELTA GENES AND USES THEREOF
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                         APPLICANT: ROSELLE GENOMICS LTD
APPLICANT: ROSELLE GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PATENTIN VERSION 3.2
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                                                                                                                                            CT-US02-38216-46976
Sequence 46976, Application PC/TUS0238216
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
PCT-US02-38216-26689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-46976
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Matches 15; Conserv
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LENGTH: 22
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LENGTH: 19
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Sequence 18418.

Sequence 18418.
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GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
LENGTH: 20
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Sequence 51847, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 51847
LENGTH: 21
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Pred. No. 1.7e+04;
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Pred. No. 1.7e+04;
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Best Local Similarity 88.2%;
Matches 15; Conservative (
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Best Local Similarity 88.2%;
Matches 15, Conservative
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/ ORGANISM: Homo sapiens
PCT-US02-38216-18418
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CRGANISM: Homo sapiens
PCT-US02-38216-39237
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; ORGANISM: Homo sapiens
PCT-US02-38216-51847
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PCT-US02-38216-51847
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PCT-US02-38216-47426
; Sequence 47426
; Sequence 47426
; GENERAL INFORMATION:
; APPLICANT: ROSetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY;
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.2
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Sequence 61865, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
TITLE OF INVENTION: GENES AND USES THEREOF
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 61865
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         GENES AND USES THEREOF
TITLE OF INVENTION: GENES AND USES THEREOFFILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 18278
LENGTH: 19
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; ORGANISM: Homo sapiens
PCT-USO2-38216-61865
                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
PCT-US02-38216-18278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
PCT-US02-38216-47426
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LENGTH: 19
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Sequence 63940, Application PC/TUS0238216

Sequence 63940, Application PC/TUS0238216

GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 63940
LENGTH: 22
                                                                                                                                                                                                                                                                               Sequence 75562, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 75562
LENGTH: 21
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Query Match 76.7%; Score 13.8; DB 1; Length 21; Best Local Similarity 88.2%; Pred. No. 1.6e+04; Matches 15; Conservative 0; Mismatches 2; Indels
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CORGANISM: Homo sapiens
PCT-US02-38216-75562
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PCT-US02-38216-63940
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Search completed: October 27, 2003, 18:22:55 Job time : 308.029 secs

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253.343 Million cell updates/sec
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| cgn2_6/ptodata/1/pna/PTUS_COMB.seq:*
| cgn2_6/ptodata/1/pna/US06_COMB.seq:*
| cgn2_6/ptodata/1/pna/US08_COMB.seq:*
| cgn2_6/ptodata/1/pna/US09_COMB.seq:*
| cgn2_6/ptodata/1/pna/US09_CO
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                      nucleic search, using sw model
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Perfect score:
Sequence:
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6/ptodata/1/pna/US101B_COMB.seq:*
6/ptodata/1/pna/US101B_COMB.seq:*
6/ptodata/1/pna/US6002_COMB.seq:*
6/ptodata/1/pna/US6002_COMB.seq:*
6/ptodata/1/pna/US6003_COMB.seq:*
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6/ptodata/1/pna/US6012_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Sequence 3, Appli	Seguence 1, Appli	Seguence 4, Appli	Sequence 17, Appl
ID	7-0	19 US-09-331-204-1	US-09-331-204A-4	US-09-786-436-17
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Query Match Length DB	m	18	18	18
Query Match	18 100.0	100.0	100.0	100.0
Score	87	18	18	18
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US-09-331-204A-4

Sequence 4, Application US/09331204A

Sequence 4, Application US/09331204A

GENERAL INFORMATION:

APPLICANT: ICN Pharmaceuticals, Inc.

APPLICANT: Tam, Robert

TITLE OF INVENTION:

G-rich Oligo Aptamers and Methods of Modulating an Immune Resy

FILE REFERENCE: 216/013-US1

CURRENT APPLICATION NUMBER: BCT/US97/23927

PRIOR APPLICATION NUMBER: PCT/US97/23927

PRIOR APPLICATION NUMBER: PCT/US97/23927

PRIOR FILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.0

SEQ ID NO 4

LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09331204
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN TITLE OF INVENTION: IMMUNE RESPONSE
FILE REFERENCE: ICNSequence
CURRENT APPLICATION NUMBER: US/09/331,204
CURRENT APPLICATION NUMBER: PCT/US97/23927
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR APPLICATION NUMBER: PCT/US97/23927
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 1
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 18;
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Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 0;
8250-011
             TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-854-3660
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                       US-08-387-041A-3
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Sequence 6, Application US/09331204

GENERAL INFORMATION:
APPLICANT: Tam, Robert
TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
TITLE OF INVENTION: IMMUNE RESPONSE
FILE REFERENCE: ICNSequence
CURRENT APPLICATION NUMBER: US/09/331,204
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR PILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
LENGTH: 21
                                                                                                                                                                                                                                           GENERAL INFORMATION:

Sequence 4, Application US/08387041A
GENERAL INFORMATION:

APPLICANT: Tam, Robert C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION
NUMBER OF SEQUENCES: 41
CORRESSEE: Pannie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/387,041A
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 25,227
REFE
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100.0%; Score 18; DB 8; 1
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 0;
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MOLECULE TYPE: DNA (genomic)
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US-09-331-204-6
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Sequence 42, Application US/09786436
Sequence 42, Application US/09786436
Sequence 42, Application US/09786436
APPLICANT: Heeg, Klaus
TITLE OF INVENTION: G-Motif Oligonucleotides and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: C1041/7010 (Aws)
CURRENT APPLICATION NUMBER: US/09/786,436
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: PCT/EP99/06502
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 42
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hermann
APPLICANT: Lipford, Grayson
APPLICANT: Heeg, Klaus
TITLE OF INVENTION: G-Motif Oligonucleotides and Uses
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
TITLE REFERENCE: C1041/7010 (Aws)
CURRENT APPLICATION NUMBER: US/09/786,436
CURRENT FILING DATE: 2001-03-02
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 18; DB 33; Best Local Similarity 100.0%; Pred. No. 4.8e+03; Matches 18; Conservative 0; Mismatches 0;
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; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-4
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ORGANISM: Artificial Sequence
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US-09-786-436-42/c
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US-09-786-436-17
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Sequence 7, Application US/09331204A

Sequence 7, Application US/09331204A

GENERAL INFORMATION:

APPLICANT: ICN Pharmaceuticals, Inc.

APPLICANT: Tam, Robert

TITLE OF INVENTION:

FILE REFERENCE: 216/013-013

FILE REFERENCE: 216/013-014

CURRENT APPLICATION NUMBER: US/09/331,204A

CURRENT FILING DATE: 1999-08-20

PRIOR FILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                              JOSTON STATE OF THE STATE OF STATE OF STATE OF STATE OF STATE OF MODIFICATION:

APPLICANT: ICN Pharmaceuticals, Inc.
APPLICANT: Tam, Robert
TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Res;
FILE REFERENCE: 216/013-US1
CURRENT FILING DATE: 1999-08-20
PRIOR FILING DATE: 1997-12-19
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
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216/013-US1
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        Indels
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Pred. No. 1.9e+04;
0; Mismatches 1;
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Pred. No. 7.8e+04;
0; Mismatches 2;
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APPLICANT: ICN Pharmaceuticals, Inc.; APPLICANT: Tam, Robert; TITLE OF INVENTION: G-rich Oligo Ap; FILE REFERENCE: 216/013-US1
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88.9%;
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Best Local Similarity 94.4%;
Matches 17; Conservative
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US-09-331-204A-7
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Best Local Similarity 88.9%
Thes 16, Conservative
        17; Conservative
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GENERAL INFORMATION:
APPLICANT: ICN Pharmaceuticals, Inc.
APPLICANT: Tam, Robert
TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Responsible File Reference: 216/013-US1
CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Version 3.0
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TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
TITLE OF INVENTION: IMMUNE RESPONSE
FILE REFERENCE: ICNSequence
CURRENT APPLICATION NUMBER: US/09/331,204
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR RILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 18
                                            ) OTHER INFORMATION: Description of Artificial Sequence: An oligomer; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic; OTHER INFORMATION: acid. This term includes oligomers consisting of; OTHER INFORMATION: naturally occurring bases, sugars and intersugar (US-09-331-204-6
                                                                                                                                                                                                                                                Gaps
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Pred. No. 1.9e+04;
                                                                                                                                                                                                                                              0; Indels
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100.0%; Score 18; DB 19;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                            Query Match 100.0%; Score 18; DB 19; Best Local Similarity 100.0%; Pred. No. 4.8e+03; Matches 18; Conservative 0; Mismatches 0;
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94.4%;
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SEQ ID NO 6
; LENGTH: 21
; TYPE: DNA
; ORGANISM: synthetic construct US-09-331-204A-6
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Best Local Similarity
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APPLICANT: NOSELTAGEMONICS
APPLICANT: RESCULATORY GEN
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 38943
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 19;
             Length 18;
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         Score 14.4; DB 50;
Pred, No. 1.1e+05;
); Mismatches 1;
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Job time : 2357.29 secs
                                                                                                                                                                                                                                      US-10-310-188-38943
; Sequence 38943, Application US/10310188
; GENERAL INFORMATION:
                                                                                                     3 GGAGGGGGTGGTGGGG 18
                                                                                                                                              1 GGAGGGGTGGAGGGG 16
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93.8%;
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Best Local Similarity 93.8
Matches 15; Conservative
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         Query Match
Best Local Similarity
Matches 15; Conserv
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US-10-310-188-41647
Sequence 41647, Application US/10310188
GENERAL INFORMATION:
APPLICANT: ROSettaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
TITLE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
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TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
TITLE OF INVENTION: IMMUNE RESPONSE
FILE REFERENCE: ICNSequence
CURRENT APPLICATION NUMBER: US/09/331,204
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: An oligomer of There in OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic OTHER INFORMATION: acid. This term includes oligomers consisting of OTHER INFORMATION: naturally occurring bases, sugars and intersugar (US-09-331-204-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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CURRENT APPLICATION NUMBER: US/09/331,204A CURRENT FILING DATE: 1999-08-20 PRIOR APPLICATION NUMBER: PCT/US97/23927 PRIOR FILING DATE: 1997-12-19 NUMBER OF SEQ ID NOS: 28 SOFTWARE: Patentin version 3.0 SEQ ID NO 9 LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-09-331-204-4
; Sequence 4, Application US/09331204
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                             ) ORGANISM: synthetic construct US-09-331-204A-9
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CORGANISM: Homo sapiens
US-10-310-188-41647
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LENGTH: 18
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FNGTH: 19
                                                                                                                                                                                          TYPE: DNA
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October 27, 2003, 11:25:34 ; Search time 387.943 Seconds (without alignments) 124.432 Million cell updates/sec
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cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
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cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
cgn2_6/ptodata/1/pubpna/USO0A_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1792395 segs, 1340900451 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                              OM nucleic - nucleic search, using sw model
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18
1 ttggaaggggtggtgggg 18
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Maximum DB seq length: 22
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

equence 22, equence 533 equence 904 equence 4, equence 9, ouence 174,	Sequence 10, Sequence 56, Sequence 36, Sequence 56, equence 11,	quence 30, quence 31, equence 59, equence 22, equence 22, equence 22,		equence 117 equence 117 equence 67, equence 67,
-09-988-115A- -10-032-585-5 -09-263-959-9 -10-196-660-4 -10-318-628-9	S-09-755-004- S-09-779-152- S-09-767-421- S-10-023-610-	US-09-828-034-30 US-09-828-034-31 US-10-204-884-59 US-10-059-877-22 US-10-059-888-22 US-09-263-959-90	30-423-5 30-423-5 45-237A-6 61-201-1 61-201-1 61-201-1	US-09-846-0338-1 US-10-006-069A-1 US-10-010-920-67 US-10-008-721-67
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Sequence 2132, Application US/09817879; Publication No. US20030171311A1; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Hepatitis C Virus Infection
TITLE OF INVENTION: Hepatitis C Virus Infection
TITLE OF INVENTION: WBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
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Pred. No. 2e+04;
2; Mismatches 0; Indels
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Pred. No. 2e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: RPI 400/003
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: Patentin version 3.0
SEQ ID NO 2423
LENGTH: 17
                                                                         NAME/KEY: misc_feature; LOCATION: CTHER INFORMATION: oligonucleotide substrate; US-09-740-332-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION:
; OTHER INFORMATION: Oligonucleotide substrate
US-09-740-332-2423
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NAME/KEY: misc_feature

LOCATION:

OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2132
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         TYPE: RNA ORGANISM: artificial sequence
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ORGANISM: artificial sequence
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Best Local Similarity 84.6%;
Matches 11; Conservative
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Best Local Similarity 84.6
Matches 11; Conservative
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US-09-817-879-2132/c
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LENGTH: 17
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TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate TITLE OF INVENTION: Hepatitis C Virus Infection FILE REFERENCE: RPI 400/003 CURRENT APPLICATION NUMBER: US/09/740,332 CURRENT FILING DATE: 2001-03-26 NUMBER OF SEQ ID NOS: 9704 SOFTWARE: Patentin version 3.0 SEQ ID NO 2132 LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 213.

Sequence 22.

Sequence 22.

Sublication No. US20030125270A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals Inc.

APPLICANT: Ribozyme Pharmaceuticals Inc.

TITLE OF INVENTION: Hepatitis C virus Infection

FILE REFERENCE: RPI 400/003

CURRENT APPLICATION NUMBER: US/09/740,332

CURRENT FILING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 9704

SOFTWARE: Patentin version 3.0

SEQ ID NO 2133

LENGTH: 17
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Publication No. US20030125270A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: RPI 400/003
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2422
LENGTH: 17
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Pred. No. 2e+04;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 72.2%; Score 13; DB 11; Length 17; Best Local Similarity 100.0%; Pred. No. 2e+04; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Oligonucleotide substrate US-09-740-332-2132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: oligonucleotide substrate US-09-740-332-2133
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Best Local Similarity 100.0%; Pr
Matches 13; Conservative 0;
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                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION:
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US-09-740-332-2133/c
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Sequence 26, Application US/10059877

Publication No. US20030157490A1

GENERAL INFORMATION:
APPLICANT: CHAO, LEE
APPLICANT: OF INVENTION: HYPERTEMSION
TITLE OF INVENTION: HYPERTEMSION
TOWNER: 09/495,140
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 1997-05-14
MUMBER OF SEQ ID NOS: 31
SCOTION OF 26
LENGTH: 17
                        Sequence 2423, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Hepatitis C Virus Infection
; TITLE OF INVENTION: Hepatitis C Virus Infection
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MBHB00-801-R; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2423
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US-10-059-877-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ), OTHER INFORMATION: Oligonucleotide substrate US-09-817-879-2423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: artificial sequence
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Best Local Similarity 84.6
Matches 11; Conservative
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NAME/KEY: misc_feature
LOCATION:
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US-10-303-109A-30/c
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US-10-059-877-26
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; Sequence 2133, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
    APPLICANT: Ribozyme Pharmaceuticals Inc.
    TITLE OF INVENTION: Hepatitis C virus Infection
    TITLE OF ERERENCE: MBHB00-801-F
    CURRENT APPLICATION NUMBER: US/09/817,879
    CURRENT FILING DATE: 2001-03-26
    NUMBER OF SEQ ID NOS: 9703
    SOFTWARE: Patentin version 3.0
    SEQ ID NO 2133
    FAMORE OF 2133
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TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13; DB 12; Length 17; Pred. No. 2e+04;
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
    Pred. No. 2e+04;
; Mismatches 0;
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) OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2133
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Publication No. US20030171311A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%; Powatches 13; Conservative 0;
Best Local Similarity 100.0%; P
Matches 13; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA ORGANISM: artificial sequence
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ORGANISM: artificial sequence
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US-09-817-879-2422
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APPLICANT: Robl, James M.
APPLICANT: Robl, Stacy E.
APPLICANT: Ferguson, Stacy E.
APPLICANT: Ferguson, Stacy E.
APPLICANT: Furciwa, Yoshima
APPLICANT: Tomizuka, Kazuma
APPLICANT: Tomizuka, Kazuma
APPLICANT: Ishida, Isao
TITLE OF INVENTION: Expression of Xenogenous (Human)
TITLE OF INVENTION: Immunoglobulins in Cloned, Transgenic Ungulates
FILE REFERENCE: 50195/008003
CURRENT APPLICATION NUMBER: US/09/988,115A
CURRENT FILING DATE: 2002-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 71.1%; Score 12.8; DB 14; Length 20; Best Local Similarity 87.5%; Pred. No. 2.3e+04; Matches 14; Conservative 0; Mismatches 2; Indels
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                                    APPLICANT: Lex M. COWSERT
TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
FILE REFERENCE: RTSP-0363
CURRENT APPLICATION NUMBER: US/10/181,846
CURRENT PILING DATE: 2002-07-17
PRIOR PILING DATE: 2002-07-17
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 176
SEQ ID NO 35
LENGTH: 20
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87.5%; Pred. No. 2.3e+04;
tive 0; Mismatches 2;
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, OTHER INFORMATION: Antisense Oligonuclectide US-10-181-846-35
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PRIOR PILING DATE: 2001-08-09
PRIOR PELING DATE: 2001-08-09
PRIOR PPLICATION NUMBER: US 60/256,458
PRIOR PPLICATION NUMBER: US 09/714,185
PRIOR APPLICATION NUMBER: US 09/714,185
PRIOR APPLICATION NUMBER: US 60/166,410
PRIOR PILING DATE: 1999-11-19
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Synthetic Primer US-09-988-115A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-988-115A-3/c; Sequence 3, Application US/09988115A; Publication No. US20030037347A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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                 APPLICANT: Nicholas M. Dean
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US-09-988-115A-13/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CHAO, ULIE
APPLICANT: CHAO, ULIE
APPLICANT: CHAO, ULLIE
APPLICANT: SONG, QING
TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL
TITLE OF INVENTION: HYPERTENSION
TITLE OF INVENTION: HYPERTENSION
FILE REFERENCE: 19113.0081U2
CURRENT APPLICATION NUMBER: US/10/059,888
CURRENT FILING DATE: 2000-01-31
PRIOR FILING DATE: 1990-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1997-05-14
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FREASEQ for Windows Version 4.0
SEQ ID NO 26
TENNATH: 17
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US-10-059-888-26
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Sequence 30, Application US/10303109A
Publication No. US20030194726A1
GENERAL INFORMATION:
APPLICANT: BOLCHAKOVA, Elena
APPLICANT: ROZZELLE; James
TITLE OF INVENTION: Thermus Oshimai Nucleic Acid Polymerases
CURRENT APPLICATION NUMBER: US/10/303,109A
CURRENT FILING DATE: 2002-11-22
PRIOR FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.2
SEQ ID NO 30
LENGTH: 17
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US-10-059-888-26
; Sequence 26, Application US/10059888
; Publication No. US20030025882A1
; GENERAL INFORMATION:
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71.1%; Sci
Best Local Similarity 87.5%; Pri
Matches 14; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-303-109A-30
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US-10-181-846-35
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Search completed: October 27, 2003, 19:00:52 Job time : 387.943 secs

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100.0%; Score 18; DB 2; Length 18; ilarity 100.0%; Pred. No. 24; Conservative 0; Mismatches 0; Indels
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Fatent No. 5932556
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Crockett & Fish
                US-08-486-513-2
US-08-486-515-2
US-08-486-885-2
US-08-486-885-2
US-08-486-536-2
US-08-486-536-2
US-08-486-513-9
PCT-US95-11234-2
US-08-486-515-3
US-08-890-980-56
US-08-890-980-56
US-08-890-980-56
US-08-890-980-56
US-08-486-885-3
US-08-486-536-3
US-08-486-56-56
US-08-486-536-3
US-08-486-536-3
US-08-486-536-3
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC -DOS/MS-DOS SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/529,878B FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION: NAME: Fish, Robert D. REGISTRATION NUMBER: 33,880
REFERENCE/DOCKET NUMBER: 213/003
TELEPHONE: 714-525-3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Crockett & Fish
3000 S. Augusta Court
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SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
 TYPE: nucleic acid
STRANDEDNESS: unkno
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Best Local Similarity
Matches 18; Conserv
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US-08-529-878B-3
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                                                                                                                                                    October 27, 2003, 10:32:34; Search time 41.3143 Seconds (without alignments) 192.304 Million cell updates/sec
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Sequence 4, 7
Sequence 4, 7
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Sequence 1
Sequence 4
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-529-878B-4
US-08-529-878B-4
US-08-529-878B-4
US-08-476-712-2
US-09-495-140-2
US-09-495-140-2
US-09-495-140-2
US-09-490-692-35
US-09-490-692-35
US-09-490-692-35
US-09-490-692-35
US-09-809-713-3
US-08-013-801-4
US-08-072-063-13
US-08-072-063-13
US-08-072-063-13
US-08-430-417-4
US-08-46-693-13
US-08-46-693-13
US-08-46-693-13
US-08-46-693-13
US-08-46-693-13
US-08-46-693-13
US-08-46-693-13
US-08-46-822-4
US-08-704-504-4
US-08-323-342-4
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                                                                                                                                                                                                                                                                                                                                                                                                       569978 seqs, 220691566 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listing first 45 summaries
                                                                                                         - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                     1 ttggagggggtggtgggg 18
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                                                                                                                                                                                                                                              US-09-331-204A-4
18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length: 0
length: 22
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Match
                                                                                                                                                                                                                                            Title:
Perfect score:
Sequence:
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Maximum DB seq
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Database :

Searched:

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Gaps

· 0

us-09-331-204a-4.szlm22.rni

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Gaps
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| Sequence 45, Application US/08529878B
| Sequence 45, Application US/08529878B
| Patent No. 5932556
| GENERAL INFORMATION:
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
| TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
| TOTLE OF INVENTION: A BUTCH OF CD28 EXPRESSION
| TOTLE OF INVENTION: A BUTCH OF COURT O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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100.0%; Score 18;
Best Local Similarity 100.0%; Pred. No. ;
Matches 18; Conservative 0; Mismatche
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fish, Robert D.
REGISTRATION NUMBER: 33,880
REFERENCE/DOCKET NUMBER: 213/003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
13-SEP-1995
                        APPLICATION NUMBER: US/08/529,878B FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fish, Robert D.
REFERRATION NUMBER: 33,880
REFERENCE/DOCKET NUMBER: 213/003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-525-3433
TELEFAX: 714-525-3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 rrdaAdddddrdcrdcrdcdd 21
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MOLECULE TYPE: DNA (genomic)
US-08-529-878B-4
                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS LENGTH: 21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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TELEFAX: 714-525-3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: unkn
                                                                                                                                                                                                                                                                                                                                                               TELEX:
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                                      Sequence 44, Application US/08529878B

Sequence 44, Application US/08529878B

Patent No. 5932556

GENERAL INFORMATION:
APPLICANT: Tam, Rebert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES, 48

CORRESPONDENCE ADDRESS:
ADDRESSEE: Crockett & Fish
STATE: California
COUNTRY: La Habra
STATE: California
COUNTRY: United States of America
STATE: California
COUNTRY: United States of America
STATE: California
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fish, RODERT 10195
REFERENCE/DOCKET NUMBER: 213/003
TELECOMMUNICE: 714-525-3303
TELEFAX: 714-525-3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 18;
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Patent No. 5932556
GENERAL INFORMATION:
APPLICANT: Tam, Robert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Crockett & Fish
STREET: 3000 S. Augusta Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 18; DB
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches
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CITY: La Habra
STATE: California
COUNTRY: United States of America
ZIP: 90631
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: DNA (genomic)
US-08-529-878B-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                        RESULT 2
US-08-529-878B-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-529-878B-4
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Length 21;

DB 2;

100.0%; Score 18;

DNA (genomic)

, MOLECULE TYPE: US-08-529-878B-45

Query Match

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Score 13.4; DB 4;
Pred. No. 1.7e+03;
0; Mismatches 1;
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MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-411-291-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
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ORGANISM: Artificial Sequence
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Best Local Similarity 87.5%;
Matches 14; Conservative C
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Best Local Similarity 93.3
Matches 14; Conservative
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                                    Gaps
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Patent No. 5962426

GENERAL INFORMATION: Triple-Helix Forming Oligonucleotides for TITLE OF INVENTION: Targeted Mutagenesis

TITLE OF INVENTION: Targeted Mutagenesis

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSE: Patrea L. Pabst
STREET: 2800 One Allantic Center
STREET: 2010 West Peachtree Street
CITY Atlanta
STREET: 1201 West Peachtree Street
CITY: Atlanta
STREET: 130309-4450

COMPUTER: Proppy disk
COMPUTER: Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
US-09-411-291-2
; Sequence 2, Application US/09411291
; Patent No. 6303376
; GENERAL INFORMATION:
; TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for Targeted Mutagenesis
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
  Pred. No. 24; Mismatches
Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
                                                                                       1 TTGGAGGGGGTGGTGGGG 18
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Best Local Similarity 93.39
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 20 bases
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) TOPOLOGY: linear;

MOLECULE TYPE: DNA

US-08-476-712-2
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RESULT 7

US-09-495-140-26

Sequence 26, Application US/09495140

Sequence 26, Application US/09495140

Sequence 26, Application US/09495140

Sequence 26, Application US/09495140

GENERAL INFORMATION:

APPLICANT: CHAO, LEE

APPLICANT: CHAO, JULIE

APPLICANT: CHAO, JULIE

APPLICANT: CHAO, JULIE

APPLICANT: CHAO, GING

TITLE OF INVENTION: DESTENDED AND COMPOSITIONS FOR CORRELATING

TITLE OF INVENTION: OF ESSENTIAL HYPERTENSION

TITLE OF INVENTION: OF SESENTIAL HYPERTENSION

TITLE OF INVENTION NUMBER: US/09/495,140

CURRENT APPLICATION NUMBER: 09/389,566

EARLIER APPLICATION NUMBER: 09/389,566

EARLIER FILING DATE: 1997-05-14

NUMBER OF SEQ ID NOS: 31

SEQ ID NO 26

LENGTH: 17
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COTHER INFORMATION: Description of Artificial Sequence:/No. 6376182e
COTHER INFORMATION: synthetic construct
US-09-495-140-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/411,291
FILING DATE: 04-Oct-1999
CLASSIFICATION & UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,712
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea 1.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: YUll4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 20
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Gaps
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                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
STREET: GOO Travis, Suite 1850
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: TREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: IBM PC compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: IMP PC compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: IMP PC COMPATA:
APPLICATION NUMBER: US/08/682,255A
FILING DATE: 17-JULY-1996
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: GO/014,007
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: GO/014,007
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: GO/016,271
FILING DATE: 17-APRIL-96
APPLICATION NUMBER: GO/016,271
FILING DATE: 23-APRIL-96
APPLICATION NUMBER: GO/016,271
FILING DATE: 23-APRIL-96
APPLICATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06214
TELECOMMUNICATION INFORMATION:
                  APPLICANT: Hogan, Michael E.
APPLICANT: Pommier, Eyves
APPLICANT: Mazumder, Abhijit
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 57, Application US/09429130 Patent No. 6355785 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fennewald, Susan
Zendegui, Joseph G
Ojwang, Joshua O.
Hogan, Michael E.
Pommier, Eyves
Mazumder, Abhijit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rando, Robert F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) US-08-682-255A-57
Ojwang, Joshua O.
Hogan, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 redredererered 17
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STRANDEDNESS:
TOPOLOGY: lin
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                                                                                                                                                                                                          GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Rando, Robert F.

APPLICANT: Ojwang, Joshua O.

APPLICANT: Ojwang, Joshua O.

APPLICANT: Wallace, Thomas L.

APPLICANT: Cossum, Paul A.

TITLE OF INVENTION: Anti-Viral Guanosine-Rich

TITLE OF INVENTION: Anti-Viral Guanosine-Rich

TITLE OF INVENTION: Anti-Viral Guanosine-Rich

CORRESPONDENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Conley, Rose & Tayon, P.C.

STREET: 600 Travis, Suite 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: nouscours
STATE: nouscours
COUNTRY: U.S.A.
ZIP: 7702-2912
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WOOD DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/017,974
FILING DATE: 04-FEB-97
APPLICATION NUMBER: 60/037,374
FILING DATE: 04-FEB-97
APPLICATION NUMBER: 60/037,374
FILING DATE: 09-DEC-97
APPLICATION NUMBER: 1472-06223
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
REFERENCE/DOCKET NUMBER: 1472-06223
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/238-8010
TELEPHONE: 713/238-8010
TELEFAX: 713/238-8010
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APPLICANT: Rando, Robert F. APPLICANT: Fennewald, Susan APPLICANT: Zendegui, Joseph G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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US-08-682-255A-57
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RESULT 13
US-09-199-542B-19
; Sequence 19, Application US/09199542B
; Patent No. 6479235
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Sprecher, Cynthia J.
; TITLE OF INVENTION: Multiplex Amplification of Short Tandem Repeat Loci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Madison
STATE: Wisconsin
COUNTRY: U.S.A.
ZIP: 33711-5399
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
COMPUTER: IBM compatible PC
OPERATING SYSTEM: DOS, version 6.0
SOFTWARE: WordPerfect 5.1 (Dos text format)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,575B
FILING DATE: 04/15/96
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/316,544
FILING DATE: 09/30/94
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 21
TWOP: Nucleic Acid
                                                                                                                                                                                                            Score 12.8; DB 3;
Pred. No. 3.1e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 71.1%; Score 12.8; DB 2; Best Local Similarity 87.5%; Pred. No. 3.1e+03; Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Schumm, James W.
TITLE OF INVENTION: Multiplex Amplification of
TITLE OF INVENTION: Short Tandem Repeat Loci
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Promega Corporation
STREET: 2800 Woods Hollow Road
CITY: Madison
                                                                             TYPE: DNA
CRGANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: Antisense Oligonucleotide
US-09-490-692-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Application US/08632575B Patent No. 5843660
                                                                                                                                                                                                             Query Match
Best Local Similarity 87.5%;
Matches 14; Conservative C
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MAP POSITION: D14S562
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STRANDEDNESS: Single
TOPOLOGY: Linear
              NUMBER OF SEQ ID NOS: 176
SEQ ID NO 35
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-08-632-575B-19
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Patent No. 6180353
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
FILE REFERENCE: RTS-0120
CURRENT APPLICATION NUMBER: US/09/490,692
CURRENT FILING DATE: 2000-01-24
                                                                          NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
STREET: 600 Travis, Suite 1850
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77002-22NE
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: MS Word 97 (saved as .txt file)
60/015,714
TITLE OF INVENTION: Anti-Viral Guanosine-Rich Oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: MCDANIEL, C. Steven
REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06214
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/238-8010
TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                     SNT APPLICATION DATA:
APPLICATION NUMBER: US/09/429,130
FILING DATE: 28-Oct-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/682,255
FILING DATE: <Unknown>
APPLICATION NUMBER: 60/001,505
FILING DATE: 19-JULY-95
APPLICATION NUMBER: 60/014,007
FILING DATE: 25-MARCH-96
APPLICATION NUMBER: 60/013,688
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 17-APRIL-96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
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25-MARCH-96
19-MARCH-96
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23-APRIL-96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 TGGAGGGGGTGGTGGG 17
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US-09-490-692-35
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Search completed: October 27, 2003, 14:03:33 Job time: 42.3143 secs
      Illinois
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; Sequence 4, Application US/08013801
; Patent No. 5420019
; GENERAL INFORMATION:
    APPLICANT: Theofan, Georgia
    APPLICANT: Horwitz, Arnold
    APPLICANT: Burke, David
    APPLICANT: Bu
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; OTHER INFORMATION: probe upstream of the 1450 point mutation region
US-09-809-713-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 71.1%; Score 12.8; DB 4; Length 21; Best Local Similarity 87.5%; Pred. No. 3.1e+03; Matches 14; Conservative 0; Mismatches 2; Indels
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Bicknell
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Patent No. 6428964
GENERAL INFORMATION:
APPLICANT: Shuber, Anthony
TITLE OF INVENTION: Method For Alteration Detection
FILE REFERENCE: EXT-047
CURRENT APPLING DATE: 2001-03-15
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.0
FILE REFERENCE: 16026/9212
CURRENT APPLICATION NUMBER: US/09/199,542B
CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: US 08/316,544
PRIOR APPLICATION NUMBER: US 08/316,544
PRIOR FILING DATE: 1994-09-30
PRIOR FILING DATE: 1996-04-15
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Word97 (converted to DOS text format)
SEQ ID NO 19
LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapien
LOCATION: D148562
US-09-199-542B-19
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US-08-013-801-4
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US-09-809-713-3
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                                                                                                          CPERATING SISIEM: PC-DOS/M3-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/013,801
FILING DATE: 02 FEB 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 27129/30911
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFHONE: 312/346-5750
TELEFRAX: 312/346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.8%; Score 12.2; DB 1;
82.4%; Pred. No. 5.3e+03;
trive 0; Mismatches 3;
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312/346-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA
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Fax: 801 585 7177
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AZ760597 1M0554N21
AZ512326 1M0357118
AZ645269 1M0510B10
                                                                                                                                                                                                 October 27, 2003, 10:32:29; Search time 1581.77 Seconds (without alignments) 276.576 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22781392 seqs, 12152238056 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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19 28 AZ760597
20 28 AZ512326
20 28 AZ645269
                                                                                                                               OM nucleic - nucleic search, using sw model
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18
1 ttggaggggtggtgggg 18
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Z659755 1M0537F2	Z969440 2M024201	A2583408 1M03/8NZ3 A2774703 2M0004G14	Z969578 2M0242G2	Z307952 1M0010L2	Z645874 1M0511C0	Z769521 1M057001	Z871408 2M0184E1	Q901245 hasp002x	251781 qu76g01.x	Z315293 1M0032P2	Z622226 1M045E	Z666896 1M0549A2	Z856540 2M0161D0	568336 tn68h08	Z766712 1M0564	Z876923 2M0192D0	364573 qw37g03	AZ476392 1M0295F1	Z512534 1M0358	I183338 qd41a12	I434548 ti49d05	582080 ar96b07	I735392 at10e10	Q585098 E011826-	Z331988 1M0060B1	Z607348 1M0429D1	Z391065 1M0152H2	Z430735 1M0215A2	Z845320 2M0145	Z995847 2M0281N1	21051 HUMGS020	Z792883 ZM0045	I590540 twllc02	807936 wf52e09	Z369361 1M011912	Z381798 1M0138G0	Z447936 1M024501	Z780591 2M0018	Z405596 1M0174B0	
28 AZ65975	28 AZ96944	1 28 AZ383408 1 28 AZ774703	28 AZ96957	28 AZ30795	28 AZ64587	28 AZ76952	28 AZ87140	13 BQ90124	9 AI251781	28 AZ31529	28 AZ6222	28 AZ66689	28 AZ85654	9 AI568336	28 AZ76671	28 AZ8769	9 AI364573	28 AZ47639	28 AZ5125	9 AI183338	9 AI43454	9 AI58208	9 AI73539	13 BQ58509	28 AZ33198	28 AZ60734	28 AZ39106	28 AZ43073	28 AZ84532	28 AZ9958	14 D21051	28 AZ79288	9 AIS90540	9 AI80793	28 AZ36936	28 AZ38179	28 AZ44793	28 AZ780	28 AZ40559	
2.8 71.1 2	71.1 2	12.8 71.1 21	2.8 71.1 2	2.8 71.1 2	2.8 71.1 2	2.8 71.1 2	2.8 71.1 2	2.2 67.8 1	2.2 67.8 1	2.2 67.8 1	2.2 67.8 2	2.2 67.8 2	2.2 67.8 2	2.2 67.8 2	2.2 67.8 2	2.2 67.8 2	1.8 65.6 1	1.8 65.6 2	1.8 65.6 2	1.8 65.6 2	1.8 65.6 2	1.8 65.6 2	1.8 65.6 2	1.8 65.6 2	1.8 65.6 2	1.8 65.6 2	1.6 64.4 2	1.6 64.4 2	1.6 64.4 2	1.6 64.4 2	1.6 64.4 2	1.6 64.4 2	1.4 63.3 1	1.4 63.3 1	1.4 63.3 1	1.4 63.3 1	1.4 63.3 1	1.4 63.3 1	1.4 63.3 2	
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ALIGNMENTS

AZ468862	
LOCUS	AZ468862 21 bp DNA linear GSS 04-OCT-2000
DEFINITION	1M0282004F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
	clone UUGC1M0282004 F, genomic survey sequence.
ACCESSION	AZ468862
VERSION	AZ468862.1 GI:10626987
KEYWORDS	. ღ.ფ.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
	Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
	, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
	and Wright, D., Weiss, R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
	plasmid inserts
JOURNAL	Unpublished
COMMENT	Contact: Robert B. Weiss
	University of Utah Genome Center
	University of Utah
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
	84112, USA
	Tel: 801 585 5606

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VERSION
KEYWORDS
SOURCE
ORGANISM
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AZ512326/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi]4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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19 bp DNA linear GSS 16-FEB-2001

1M0554N21F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                    /sex="Male"
/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0282 row: O column: 04
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory Mouse DNA Resource
                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0282004"
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Conservative 0;
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                /clone="UGCLM035/118"
/sax="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
/http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynuclectide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
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of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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20 bp DNA linear GSS 14-DEC-2000
1M0510B10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0510B10 R, genomic survey sequence.
AZ645269
AZ645269.1 GI:11774602
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0357 row: I column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Location/Qualifiers
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AZ645269/c
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil 4732114 |gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.,
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Unpublished
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Tel: 7, 101 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0510 row: B column: 10
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIMO510B10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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AZ659755:1 GI:11796901
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Matches 14; Conserv
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AZ583408/c
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/sex="Mouse Tool strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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2M0242012F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0242012 F, genomic survey sequence.
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                  S. 2030 E., SLC,
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Rm. 308, Biomedical Polymers Research Bldg., 2084112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0537 row: F column: 22
Seg primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
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/clone="UUGC1M0537F22"
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Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
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Mus musculus
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AZ969440.1 GI:13840667
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Lac 14; Conservative
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AZ969440/c
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Integratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

CE 1 (bases 1 to 21)

RS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

M., Rose, M., Rose, R.,

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss
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1M0378N23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0378N23 F, genomic survey sequence.
AZ583408
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/lab host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus CS7BL/6J (female) was obtained from the Jackson
University of Utah
Rm. 308, Bicmedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0242 row: O column: 12
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                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 20.
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/60"
                                                                                                                                                                                                                                                                                                                                                                                                                     /db xref="taxon:10090"
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GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi]4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb blasmid inserts
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2M0004G14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0004G14 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0378 row: N column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
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High quality sequence stop: 21.
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Mus musculus (house mouse)
Mus musculus
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AZ774703.1 GI:12900261
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet:
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Best Local Similarity
Matches 14; Conserv
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AZ774703/c
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gif4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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21 bp DNA linear GSS 27-APR-2001
2M0242G20F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0242G20 F, genomic survey sequence.
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                        Univer.

Rm. 308, Biomeance.

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0004 row: G column: 14

Seq primer: CGTTGTAAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

- misculus"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwD42 (gill4)gh]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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AZ645874
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,

and Wright, D., Weiss, R.
                        Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                              Tell 80 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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plasmid inserts
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AZ645874/c
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                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
High quality sequence stop: 21.
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1M0010L24F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0010L24 F, genomic survey sequence.
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musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 22)
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Mouse whole genome scaffolding with paired end reads from 10kb
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Mus musculus
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Mus musculus (house mouse)
Mus musculus
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                 / organism="Mus musculus"
// morganism="Mus musculus"
// morganism="Mus musculus"
// morganism="Genomic DNA"
// strain="C57BL/6J"
// db xref="Laxon:10090"
// clone="UUGCIMO511CO7"
// sex="Male"
// lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
// clone="UuGCIMO511CO7"
// musculus C57BL/6J (male) was obtained genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
// http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwp42 (gi|4732114|gp|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli xL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1M0570018F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0570018 F, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
                                                                                                                                                S. 2030 E., SLC,
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished
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Conjubrished
Conjubrished
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bld
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert. Length: 10000 Std Error: 0.00
Plate: 0511 row: C column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
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AZ769521.1 GI:12889741
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AZ769521/c
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/ Jab host="E. Coli strain XLIO-Gold, TI-resistant, F-"
/ Jab host="E. Coli strain XLIO-Gold, TI-resistant, F-"
/ Jab host="E. Coli strain XLIO-Gold, TI-resistant, F-"
/ Jab host="E. Coli strain yellocim library"
/ Jab host="Vector: PWD42nv; Purified genomic DNA from M.
/ Muscallus CSTBL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
/ Attp://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
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adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
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purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
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22 bp DNA linear GSS 21-FEB-200
2M0184E16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0184E16 F, genomic survey sequence.
                                                                                                                                                                                                                                                        SLC,
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0570 row: O column: 18
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
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/db_xref="taxon:10090"
/clone="UUGC1M0570018"
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14; Conservative
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AI251781/c
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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hasp002xj21f Heterobasidion annosum - Scots pine infection stage subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion annosum cDNA clone hasp002xj21f, mRNA sequence.
   von Niederhausern, A.
                                                                                                                                                                              SLC,
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern, and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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0
                                                              plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
84112, USA
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Pinus sylvestris/Heterobasidion annosum
Eukaryota, mixed EST libraries.
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Asiegbu, F.O., Nahalkova, J. and Dean, R.A.
                                                                                                                                                                                                                   Tel: 801 585 5606

Eax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0184 row: E column: 16

Seg primer: CGTTGTAAAACGACGGCCAGT

Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'db_xref="taxon:10090"
'clone="UUGC2M0184E16"
                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 22.
Location/Qualifiers
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BQ901245.1 GI:22300029
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/ reganism="Pinus sylvestris/Heterobasidion annosum"
/mol_type="mRNA"
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/note="Vector: pT-Adv; Site 1: BcoRI; The subtractive hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of Heterobasidon annosum (FPS)."
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IMAGE:1978032 3'
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qu76g01.x1 NCI CGAP Brn35 Homo sapiens cDNA clone IMAGE:1978032 3 similar to TR:023949 Q39949 HYDROXYPROLINE-RICH PROTEIN. ;, mRNA
Selected Expressed sequence tags of cDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with seedling roots of Scots pine (Pinus sylvestris) Unpublished Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026, S-750 07, Uppsala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1978032"

/tissue_type="tumor, 5 pooled (see description)"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Brn35"

/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Sall;
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1 (bases 1 to 19)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
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Pred. No. 1.2e+06;
0; Mismatches 3;
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                                                                                                                                                                                                                           Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
Seq primer: T7 primer.
Location/Qualifiers
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AIZ51781.1 GI:3848310
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us-09-331-204a-4.szlm22.rst

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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.33 kb. Tumor types include: meningioma, oligodendroglioma, astrocytoma (grade II), medulloblastoma, astrocytoma (grade IV). Life Technologies catalog #: 11544-012"
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4 a

BASE COUNT ORIGIN

0; Gaps Query Match 67.8%; Score 12.2; DB 9; Length 19; Best Local Similarity 82.4%; Pred. No. 1.2e+06; Matches 14; Conservative 0; Mismatches 3; Indels

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1 TTGGAGGGGGTGGTGGG 17

17 TTGGGGGGGGGGGGG 1

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Search completed: October 27, 2003, 13:59:22 Job time: 1585.77 secs

- Acres

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October 27, 2003, 10:32:29; Search time 376.114 Seconds (without alignments) 1957.844 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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REFERENCE AUTHORS TITLE JOURNAL		8 0 G	B., Heeigonucl	9, X 7-7	and Wagner,H. des and uses thereof 17 16-MAR-2000;	
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/organism="unknown"
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Glazer,P.M.
Triple-helix forming oligonucleotides for targeted mutagenesis
Patent: US 5962426-A 2 05-OCT-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 Lipford, G.B., Heeg, K. and Wagner, H.
G-motif oligonuclectides and uses thereof
Patent: WO 0014217-A 42 16-MAR-2000;
LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ; WAGNER HERMANN (DE)
CPG IMMUNOPHARMACEUTICALS GMBH (DE)
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Location/Qualifiers
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Sequence 42 from Patent WO0014217.
AX023427
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Sequence 2 from patent US 5962426.
AR078333
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Glazer,P.M.
Methods of targeted mutagenesis using triple-helix forming
oligonucleotides
Patent: US 6303376-A 2 16-OCT-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chang,C.
Methods and compositions for predicting prostate cancer
Patent: WO 0210452-A 17 07-FEB-2002;
University of Rochester (US)
Location/Qualifiers
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74.4%; Score 13.4; DB 6; Length 20; 93.3%; Pred. No. 3.4e+05; ive 0; Mismatches 1; Indels
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Pred. No. 3.4e+05;
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/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

/note="Sequence can be repeated (
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Seguence 17 from Patent WO0210452.
AX384817
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Sequence 2 from patent US 6303376.
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OS Artificial gene
OC Artificial gene
OC Artificial gene
OC Artificial gene
OC Artificial sequence; Genes.
PN JP 1993078397-A/18
PD 30-MAR-1993
PF 29-JAN-1991 JP 1991029624
PF C12N1/21,
PC C12N1/21,
PC C12N1/21,
PC C12R1:19), (C12P21/02,C12R1:19);
CC strandedness: Single;
CC topology: Linear.
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strandedness: Single,
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DP 1993078397-A/18.

Synthetic construct
artificial sequences.

1 (bases 1 to 18)

Yamazaki,C., Takasu,N., Negoro,T. and Agui,H.
THROMBOLYTIC PROTEIN
Patent: JP 1993078397-A 18 30-MAR-1993;
SUMITOMO PHARMACEUT CO LTD
                                                                                            Query Match 71.1%; Score 12.8; DB 6; I
Best Local Similarity 87.5%; Pred. No. 6.2e+05;
Matches 14; Conservative 0; Mismatches 2;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Seguence 3 from Patent WO02102824.
AX659401
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1 (bases 1 to 18)
Rando, R.F., Fennewald, S., Zendegui, J.G., Ojwang, J.O. and Hogan, M.E.
Anti-viral guanosine-rich oligonucleotides and method of treating
                  PAT 17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown.
Unknown.
Unclassified.
1 (bases 1 to 18)
Rando,R.F., Fennewald,S., Zendegui,J.G., Ojwang,J.O., Hogan,M.E.,
Pommier,Y. and Mazumder,A.
Guanosine-rich oligonucleotide integrase inhibitors
Patent: US 6355785-A 57 12-MAR-2002;
Location/Qualifiers
                                                                                                      Unknown.
Unclassified.

1 (bases 1 to 18)
Rando,R.F., Ojwaug,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
Anti-viral guanosine-rich tetrad forming oligonucleotides
Patent: US 6288042-A 57 11-SEP-2001;
Location/Qualifiers
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Sequence 57 from patent US 6355785.
AR200300
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AR262431.1 GI:28073862
             18 bp | Sequence 57 from patent US 6288042.
AR168831
AR168831.1 GI:17904956
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Unclassified.
E 1 (bases 1 to 21)
S Schumm, J.W., Micka, K.A. and Rabbach, D.R.
Multiplex amplification of short tandem repeat loci
AL Patent: US 5843660-A 19 01-DEC-1998;
Location/Qualifiers
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Location/Qualifiers
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87.5%; Pred. No. 6e+05;
iive 0; Mismatches 2;
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/organism="synthetic construct"
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Best Local Similarity 87.5%; Pred. No. 6e+05;
Matches 14; Conservative 0; Mismatches
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 87.5%; Pred. No. 6e+05;
              Mismatches
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Sequence 19 from patent US 6479235.
AR252818
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|/organism="unknown"
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A28676/c
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Dean,N.M. and Cowsert,L.M.
Antisense modulation of daxx expression
Patent: US 6180353-A 35 30-JAN-2001;
Location/Qualifiers
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           02102824-A 3 27-DEC-2002;
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Sequence 35 from patent US 6180353.
AR126606
AR126606.1 GI:14113199
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A20477.1 GI:1566754
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Patent: WO 9200375-A 4
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Vermicon AG (
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VERSION AR252818.1 GI:27301167
KEYWORDS
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ORGANISM Unknown.
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AUTHORS
Schumm, J.W. and Sprecher, C.J.
TITLE
Multiplex amplification of short tandem repeat loci
JOURNAL Patent: US 6479235-A 19 12-NOV-2002;
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JOURNAL Patent: US 6479235-A 19 12-NOV-2002;
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JOURNAL Patent: US 6479235-A 19 12-NOV-2002;
Corganism="unknown"
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps
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Search completed: October 27, 2003, 11:09:22 Job time : 380.114 secs

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Reduction; T cell; CD28; gene expression; treatment; immune system disorder; graft versus host disease; septic shock; viral disease; psoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR; systemic lupus erythematosus; inflammatory bowel disease; triplex forming; oligonucleotide; 5'-untranslated region; ss
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AAT36196 standard; DNA; 18
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 WO9624380-A1.
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18-SEP-1995;
09-FEB-1995;
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                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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Match Length
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length: 22
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Maximum DB seq
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WPI; 1999-443609/37.
                                 present invention.
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                                                                                                                                                                                                                                                                                                                                                  USS932556-A.
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                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                                                                                                                           AAX90290;
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AAZ99625
ID AAZ9
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AC AAZ9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                               The present oligonucleotide reduces T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematcsus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
(Updated on 25-MAR-2003 to correct PR field.)
                                                             Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8;
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                                                                                                                                                                                                                                                                                 Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD28 inhibiting phosphorothioate oligonucleotide RT03S.
                                                                                                                                                                                                                                                                               100.0%; Score 18; DB 17; 100.0%; Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                           Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; Column 21; 45pp; English.
                                                                                                             Claim 9; Page 54; 77pp; English
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                                                                                                                                                                                                                                                                                          Local Similarity 100.
es 18; Conservative
(ICNC ) ICN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphorothicate; ss.
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                                           WPI; 1996-384228/38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                                                                                                                                                                                 Query Match
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                      Tam RC;
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The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated
method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; ss.
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                                                                                                                                                                                            100.0%; Score 18; DB 20;
100.0%; Pred. No. 3.1e+02;
tive 0; Mismatches 0;
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                                                                                                                                          Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
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Matches 18; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX90290 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-SEP-1999 (first entry)
                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 18; Conservative
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G-motif oligonuclectide, vaccine, Toxoplasmosis, viral infection; antigen presenting cell activation; natural killer cell; septic shock; cytotoxic T-lymphocyte; inflammation; autoimmune disease; rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis; Kawasaki syndrome; graft-versus-host disease; transplant rejection; helper T cell response 1-mediated disease; Lyme arthritis; streptococcal induced arthritis; chronic inflammatory bowel disease; streptococcal induced arthritis; chronic inflammatory bowel disease; psoriasis vulgaris; experimental allergic encephalomyelitis; insulin-dependent diabetes mellitus; bacterial infection; tumour; ss.

Nucleotide sequence of non-G-motif oligonucleotide GRF1comp.

12-JUL-2000 (first entry)

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G-motif oligonucleotide, vaccine, Toxoplasmosis, viral infection, antigen presenting cell activation; natural killer cell; septic shock, cytotoxic T-lymphocyte; inflammation; autoimmune disease; rheumatoid arthritis; Crohn's disease; sarcoidosis, multiple sclerosis; kawasaki syndrome; graft-versus-host disease; transplant rejection; helper T cell response 1-mediated disease; Lyme arthritis; Streptococcal induced arthritis; chronic inflammatory bowel disease; psoriasis vulgaris; experimental allergic encephalomyelitis; insulin-dependent diabetes mellitus; bacterial infection; tumour; ss. parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Compositions comprising G-motif oligonucleotides useful for treating e.g. septic shock, rheumatoid arthritis, diabetes and human immunodeficiency virus infections -
                                      Nucleotide seguence of G-motif oligonucleotide GR1
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                                                                                                                                                                                                                                                                                                                                                     (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 14; Page 32; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                 Heeg K;
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                                                                                                                                                                                                                                                                                                                            98EP-0116652.
                                                                                                                                                                                                                                                                                                 99WO-EP06502
              (first entry)
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1es 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-256970/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        precursor cells.
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                                                                                                                                                                                                                                                                                                 03-SEP-1999;
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              12-JUL-2000
                                                                                                                                                                                                                                                                      16-MAR-2000
                                                                                                                                                                                                                  Synthetic.
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Compositions comprising G-motif oligonucleotides useful for treating e.g. septic shock, rheumatoid arthritis, diabetes and human immunodeficiency virus infections -

(CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

03-SEP-1998; 03-SEP-1999; 16-MAR-2000

99WO-EP06502. 98EP-0116652

WO200014217-A2

Synthetic.

Heeg K;

Wagner H, Lipford GB, WPI; 2000-256970/22.

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The present sequence represents a non-G-motif oligonucleotide of the invention. The specification describes compositions comprising G-motif oligonucleotides inhibit activation of antigen presenting cells by inhibiting the uptake of DNA by a cell, by stimulating natural killer cells, or by co-stimulating cytotoxic CT-lymphocytes. The G-motif oligonucleotides may be used for the productions of vaccines for treating septic shock, inflammation, autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease, CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease, confisease and transplant rejection), helper T cell response 1-mediated disease and transplant rejection), helper T cell response 1-mediated disease and disease, psoriasis vulgaris, Eyme arthritis, bacterial inflammatory bowel disease, psoriasis vulgaris, experimental allergic encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis), viral infections (e.g. Cytomegalovirus and human immunodeficiency virus (CTUV)-infections), spontaneous abortions and tumours. They may also be used to induce proliferation of bone marrow cells, especially macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 18; DB 21;
100.0%; Pred. No. 3.1e+02;
iive 0; Mismatches 0;
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a G-motif oligonucleotide of the invention. The specification describes compositions comprising G-motif oligonucleotides inhibit activation of antigen presenting cells by inhibiting the uptake of DNA by a cell, by stimulating natural killer cells, or by co-stimulating cytotoxic T-lymphocytes. The G-motif oligonucleotides may be used for the productions of vaccines for treating septic shock, inflammation, autoimmune diseases (e.g. rheumatoid arthritis, crohn's disease, carcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic inflammatory bowel disease, psoriasis vulgaris, experimental allergic encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis), viral infections (e.g. Cytomegalovirus and human immunodeficiency virus (HIV)-infections), spontaneous abortions and tumours. They may also be used to induce proliferation of bone marrow cells, especially macrophage
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ID AAZ99650 standard; DNA; 18
XX
AC AAZ99650;
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Gaps

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AAT36197 standard; DNA; 21

ВР. .

AAT36197

Length 18; Indels

Synthetic.

Tam RC;

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The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothioate oligonucleotide used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD28, inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
                                                                                                                                                                                                                                                                                                                               Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
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                                                                                                                                                                                                                                                                                            WPI; 1999-443609/37.
                                                                                                                                                                                                               (TAMR/) TAM R C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TAMR/) TAM R
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                   Synthetic
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                                                                                                                                                                                                                                                      Tam RC;
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                                                                                                          Reduction, T cell; CD28; gene expression, treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; psoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR; systemic lupus erythematosus; inflammatory bowel disease; triplex forming; oligonucleotide; 5'-untranslated region; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present oligonucleotide reduces T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematcisis, inflammatory bowel disease, etc. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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                                                                         Triplex forming oligo targetting CD28 5'-UTR (nt 58-78).
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95US-0529878.
95US-0387041.
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Les 18; Conservative
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18-SEP-1995;
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RESULT 7 AAX90329

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Query Match

Matches

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Length 21;

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in cytokine release. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                        Conservative
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es 17; Conserv
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Matches
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                                   The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Reduction; T cell; CD28; gene expression; treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; psoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2; systemic lupus erythematosus; inflammatory bowel disease; IL-2; production; antisense; inhibition; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated disease, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligo:nucleotide which reduces CD28 gene expression in T cells - for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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                                                                                                                                                                                                                                                                                                                                                                                    CD28 expression inhibiting oligonucleotide, RT09s.
                                                                                                                            Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
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             Column 29; 45pp; English.
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95US-0529878.
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(first entry)
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18-SEP-1995;
09-FEB-1995;
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16-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD28; inhibition; antisense oligonucleotide; interleukín 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; phosphorothioate; ss.
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                                                Length 18;
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                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD28 inhibiting phosphorothioate oligonucleotide RT09S.
                                            91.1%; Score 16.4; DB 17;
94.4%; Pred. No. 1.3e+03;
iive 0; Mismatches 1;
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Pred. No. 1.3e+03;
0; Mismatches 1;
Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;
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                                                                                                                                               1 TTGGAGGGGGTGGTGGGG 18
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AAT36242
ID AAT36242 standard; DNA; 18
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Best Local Similarity 94.4
Matches 17; Conservative
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The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction
                           disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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Reduction; T cell; CD28; gene expression; treatment; immune systemisorder; graft versus host disease; septic shock; viral disease psoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; interleukin; systemic lupus erythematosus; inflammatory bowel disease; IL-2; production; antisense; inhibition; ss
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88.9%; Pred. No. 5.2e+03;
iive 0; Mismatches 2; Indels
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Best Local Similarity 88.9
Matches 16; Conservative
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18-SEP-1995;
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                                                                                                                                              Synthetic
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                                                                                                                                    Reduction, T cell, CD28, gene expression, treatment, immune system, disorder, graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, interleukin 2; systemic lupus erythematosus, inflammatory bowel disease, IL-2; production, antisense, inhibition; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated disease, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligo:nucleotide which reduces CD28 gene expression in T cells - for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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                                                                                                    CD28 expression inhibiting oligonucleotide, RTOSs.
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18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
                                          25-MAR-2003
16-APR-1997
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16-APR-1997
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Tam RC;

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Gaps

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RESULT 12

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                                                                                                                                                The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN).

AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonucleotide used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method for inhibiting the expression
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; phosphorothicate; ss.
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                                                                                                                                                                                                                                                    Length 18;
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                                                                                                       Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
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                                                                                                                                                                                                                                                   Score 14.8; DB 20;
Pred. No. 5.2e+03;
); Mismatches 2;
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                                                                                       WPI; 1999-443609/37
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                18-SEP-1995;
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03-AUG-1999
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                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by administering an oligonucleotide polypeptide involved in gastric acid
of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in th method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gastric acid disturbance, gastric reflux, gastritis, dyspepsia, stomach ulcer, duodenal ulcer, Helicobacter pylori, antisense,
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Pred. No. 5.2e+03;
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81.2%; Pred. No. 1.5e+04;
iive 2; Mismatches 1;
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                                                                                                                                                                                                                          Sequence 18 BP; 1 A; 2 C; 11 G; 4 T; 0 other;
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88.9%;
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Matches 13; Conservative
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Best Local Similarity
Matches 16; Conserv
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DNA-RNA hybrid; ss.
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Search completed: October 27, 2003, 11:25:18 Job time : 163 secs

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October 27, 2003, 10:32:29 ; Search time 376.114 Seconds (without alignments) 1957.844 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Searched:

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		29939 Sequence	2246 Sequence	3774 Sequence	4000	3456 Sequence	3457 Sequenc	500	1112 Seguenc	1133 Sequenc	517 Sequenc	3952 Sequenc	5050 Sequence	2283	3974 Sequence	1417 Sequence	31 Antisense	7 Sequence	3523 Šeguenc	2422 Sequenc	2424 Sequenc	2425 Sequence	33 Seguence	2 C	3872 Novel p	7 Sequenc	12 sequence 2 9341 Sequence	1189 Sequenc	1949 Sequenc	Sequence 6	22 Sequence	9938 Sequence	604 Sequenc	1605 Sequenc	5458 Sequence	እ	2427 Sequence			linear PAT 29-SEP-1999						strand formation	
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PAT 11-MAY-1995
                                                                                                                          PAT 18-SEP-2002
                                                                                                                                                                                                                                unclassified.

unclassified.

E 1 (bases 1 to 20)

Wilson, A.R.B., Buckler, A., Cardon, L., Carey, A.H., Galvin, M.,

Miller, A. and North, M.

Asthma-associated gene

Patent: JP 2002500895-A 294 15-JAN-2002,

AXYS PHARMACEUTICALS INC

OS Unidentified

PN JP 2002500895-A/294

PD 15-JAN-2002

PF 21-JAN-2002

PF 21-JAN-1998 JP 2000528715

PI ANGELA R BROOKS WILSON, ALAN BUCKLER, LON

CARDON, ALISOUN H CAREY,

PI MARGARET GALVIN, ANDREW MILLER, MICHAEL NORTH

PC C12Q1/68, A01K67/027, C07K14/47, C12N15/09, C12N15/00 CC

Strandedness: Single;

CC Asthma-associated gene

FH Key Location/Qualifiers

FT source

FT source

FT F source

FT F Source

FT F Source
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Oligonucleotide DNA (33.6 AL) from patent EP0422861.
A27787
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                                                                                                                            linear
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IMPERIAL CHEMICAL INDUSTRIES PLC; ZENECA LIMITED
Location/Qualifiers
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/organism='Unidentified'
Location/Qualifiers
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74.4%; Score 13.4; DB 6;
Best Local Similarity 93.3%; Pred. No. 2.6e+05;
Matches 14; Conservative 0; Mismatches 1;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                             DNA
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/organism="unidentified"
/mol_type="genomic_DNA"
/db_xref="taxon:32644"
                                                                                                                         20 bp
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synthetic construct
artificial sequences.
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Probes
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KEYWORDS
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AUTHORS
TITLE
JOURNAL
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JOURNAL
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Unclassified.
1 (bases 1 to 20)
Brooks-Wilson, A.R., Buckler, A., Cardon, L., Carey, A.H., Galvin, M., Miller, A. and North, M.
Asthma related genes
Patent: US 6087485-A 298 11-JUL-2000;
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Single nucleotide polymorphisms in genes
Patent: WO 0118250-A 1424 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
Pharmaceuticals, Inc. (US)
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Sequence 1424 from Patent WO0118250.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Best Local Similarity 88.2%;
Matches 15; Conservative (
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Best Local Similarity 93.3
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                        Gaps
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Method and reagent for the inhibition of erg
Patent: WO 0188124-A 837 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
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Randi, A.M.
Method and reagent for the inhibition of erg
Patent: WO 0188124-A 838 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GI
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      71.1%; Score 12.8; DB 6;
87.5%; Pred. No. 4.9e+05;
7ative 0; Mismatches 2;
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Sequence 837 from Patent WO0188124.
AX422501
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Sequence 838 from Patent WO0188124.
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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AX422502.1 GI:21525884
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Query Match
Best Local Similarity 87.55
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 899 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
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Method and reagent for the modulation and diagnosis of cd2
nogo gene expression
Patent: WO 0159103-A 898 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US)
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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Pred. No. 2.6e+05;
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/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
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Seguence 898 from Patent WO0159103.
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PAT 28-AUG-2000

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BASE COUNT ORIGIN

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Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 20)
Monia, B.P. and Boggs, R.T.
Motisense oligonucleotide modulation of raf gene expression
Patent: US 595229-A 21 14-SEP-1999;
Location/Qualifiers
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87.5%; Pred. No. 4.7e+05;
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(S Cook, P. Dan. and Kawasaki, A. Mamoru.

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(AL Patent: US 6005087-A 9 21-DEC-1999;

Location/Qualifiers

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E 1 (bases 1 to 20)
S Cook, P.Dan. and Kawasaki, A.Mamoru.
2'-O-modified oligonucleotides
(AL Patent: US 5872232-A 9 16-FEB-1999;
Location/Qualifiers
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Sequence 21 from patent US 5952229.
AR073952
AR073952.1 GI:10000712
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Sequence 9 from patent US 6005087.
AR096050 GI:10024498
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                                                                                                                                                                                                                                                           unidentified
unclassified.
1 (bases 1 to 19)
Amouyel, P. and Chartier-Harlin, M.
METHOD FOR DIAGNOSING ALZHEIMER DISEASE
Patent: WO 9901574-A 2 14-JAN-1999;
INST NAT SANTE RECH MED (FR); AMOUYEL PHILIPPE (FR)
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Unclassified.
Clook, P. Dan. and Kawasaki, A. Mamoru.
2'-modified oligonucleotides
2'-modified oligonucleotides
Patent: US 5859221-A 9 12-JAN-1999;
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Sequence 9 from patent US 5859221.
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Sequence 9 from patent US 5872232.
AR036517 AR036517.1 GI:5953185
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Sequence 2 from Patent WO9901574
AX001112
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E 1 (bases 1 to 20)
S Love, W.Guy., Nicklin, P. Leslie., Hamilton, K. Ophelia. and Phillips, J. Ann.
Liposomal oligonucleotide compositions
Location/Qualifiers
Location/Qualifiers
I. 20
/organism="unknown"
NT 0 a 14 c 2 g 4 t
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                                                                           AR105507 20 bp
Sequence 7 from patent US 6096720.
AR105507 GI:12819104
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	מס מ		CD28 expression in	CD28 expression in	CD28 inhibiting ph	CD28 inhibiting ph	Triple helix third	Antisense oligonuc	Antisense oligonuc	Antisense oligonuc
	· C	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AAT36241	AAT36255	AAX90334	AAX90346	AAX14741	AAQ70343	AAQ70342	AAQ70345
	80	1	17	17	20	50	20	15	15	15
	Length	1 1 1	18	18	.18	18	17	18	21	21
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Human gene single ASTH1 gene intron/ Clone vq15 1 secre Human ASTH11 gene Primer #2 used fro	Human NOGO Inozyme	Human NOGO Inozyme Human GDMLP-1 17-m	Human GDMLP-1 17-m Human ERG hammerhe	Human ERG hammerhe	Human c-raf kinase Chimeric 2'-O-meth	Human c-raf and de	Human raf inhibito Human C-raf kinase	Oligonucleotide us	Chimeric antisense	C-rai antisense ch Human c-raf kinase	C-raf chimeric pho	Human c-raf kinase	Human FGF receptor	Human SI receptor	Human ST receptor	Human ST receptor	FGF receptor antis	Human inflammatory	Human POSHL1 scann	Human POSHL1 scann	Human POSHL1 scann	Human GDMLP-1 17-m Human GDMLD-1 17-m	Primer #16. Synth						riis.	sment: immune svs	ock; viral disease;	is, sarcoides,	is; interleu el disease;						
22 AAF96659 20 AAZ18648 21 AAA93151 21 AAA80555	3 ABK0089	4 ABN0749	4 ABN0749	4 ABK1819	7 AAT2750 8 AAX3646	8 AAT6215	8 AATS972 0 AAC1153	0 AAZ1029	0 AAX0546	0 AAX1506 1 AAA7350	1 AAZ4816	4 AAD4473	6 AAQ8873	9 AAT9948	9 AAT9948	9 AAT9948	4 AAL4675	2 AAH9175	4 ABV9121	4 ABV9122	4 ABV9122	4 ABN0749	0 AAX2309	ALIGNMENTS	8 BP.				g oligonucleotide, RT	gene expression: t	st disease, septic	s mellitus; thyroi	is; inflammatory sus; inflammatory					07.	41. 78. 41. 78.
7.4.4.4.0 12.00.00 10.00.00	11.	/T T T T T T T T T T T T T T T T T T T	.1 17	.1 17	.1	.1 20	.1	.1	.1 20	1.	.1 20	.1 20	.1 22	.1	.1 22	.1 22	.1 22	.9 15	.9	.9	.9	.9	.9 18		; DNA; 1		dat	first entry	on inhibiting	ell: CD28;	versus ho	e I diabete	erythemato	on, diction				96WO-US0150	95US-038704 95US-052987 95US-038704 95US-052987
9 13.8 76 0 13.4 74 1 13.4 74 2 13.4 74	12.8 71	12.8 71	12.8 71	12.8 71	12.8 71	12.8 71	12.8 71	12.8 71	12.8 71	12.8 71 12.8 71	12.8 71	12.8 71	12.8 71	12.8 71	12.8 71	12.8 71	12.8 71	12.4 68	12.4 68	12.4 68	12.4 68	12.4 68	12.4 68		LT 1 6241 AAT36241 standard	AAT36241;	5-MAR-2003 (1997 (CD28 expressio	tion: T c	rder, graf	iasis; typ inle soler	mulcipie sciero systemic lupus Tieze productio	1	Synthetic.	WO9624380-A1.	15-AUG-1996.	05-FEB-1996;	09-FEB-1995; 18-SEP-1995; 09-FEB-1995; 18-SEP-1995;
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of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN).
AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for inhibiting the expression
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                     (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated disease, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8;
   treating immune system diseases, e.g. graft vs. host disease.
                                                                                           The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 dene expression. useful in the
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                                                              Example 2; Page 45; 77pp; English
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                        septic shock, psoriasis, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5932556-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX90334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reduction, T cell, CD28, gene expression, treatment, immune system, disorder, graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, interleukin 2, systemic lupus erythematosus, inflammatory bowel disease,
                                                                                                                                                                                                                                          The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated disease, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligo:nucleotide which reduces CD28 gene expression in T cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD28 expression inhibiting oligonucleotide, RT06s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 18; DB 17;
100.0%; Pred. No. 3.4e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence 18 BP; 4 A; 1 C; 12 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     production; antisense; inhibition; ss
                                                                                                                                                                                                          Example 2; Page 45; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGGGAGGAGGGCTGGAA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 deddadeddeddadad 18
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95US-0529878.
95US-0387041.
95US-0529878.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT36255 standard; DNA; 18
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(first entry)
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Les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ICNC ) ICN PHARM INC
(ICNC ) ICN PHARM INC
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                                                                               WPI; 1996-384228/38
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18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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16-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT36255;
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                                         ram RC;
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Matches
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AAT36255/
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Triple helix third strand of alpha-globin gene nucleotides 827-843
                                                                                                                                                                               Hepburn AG, Wang C;
                                                                                                                                                                                                WPI; 1999-130384/11.
                   Triplex formation;
                                                       Homo sapiens
                                                                                                              22-DEC-1993;
                                                                                                                                 22-DEC-1993;
                                                                                                                                          29-OCT-1992;
                                                                         US5861244-A.
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15-FEB-1995
                                                                                          19-JAN-1999
                                              Synthetic
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AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonucleotide used in the exemplification of the
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                      CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8;
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        Length 18;
                                                                                                                                                                                                                                                                                                                                                                             Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                          Indels
                                                                                                                                                                   CD28 inhibiting phosphorothioate oligonucleotide RT06S.
        100.0%; Score 18; DB 20; 100.0%; Pred. No. 3.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 1 A; 12 C; 1 G; 4 T; 0 other;
                           Mismatches
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                                            1 GGGAGGAGGGCTGGAA 18
                                                              1 decendencedectedan 18
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                                                                                                              ВР.
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                                                                                                                                                                                                                                                                                  95US-0529878
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                                                                                                   AAX90346/c
ID AAX90346 standard; DNA; 18
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                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
                           Conservative
                                                                                                                                                                                                         phosphorothicate; ss.
                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-443609/37
                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention.
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                                                                                                                                                                                                                                                                                                                      (TAMR/) TAM R
                                                                                                                                                                                                                                                                                                    18-SEP-1995;
                                                                                                                                                 24-SEP-1999
                                                                                                                                                                                                                                                                                18-SEP-1995;
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                                                                                                                                                                                                                                             US5932556-A.
                                                                                                                                                                                                                                                              03-AUG-1999
                                                                                                                                                                                                                          Synthetic.
                                                                                                                               AAX90346;
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Н
        Query Match
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                 Best Local
Matches 1
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AAX14741/C
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Matches
                                                                                          RESULT 4
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The present sequence represents a polynucleotide that is able to form a triple helix with a double stranded sequence. Cytosine bases in the present can be replaced with 5-methylcytosine for increased triplex stability. The present sequence is used in the assay of the invention, where it can be part of the anchor DNA or reporter DNA sequence. The assay comprises adding a sample containing double-stranded DNA test sequences to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA is designed to form a triple-strand structure with part of the test sequence. Triplex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (by detecting genes for ribosomal RNA) in clinical samples, but also detection of oncogenes and Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
DNA detection; triple helix; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Pred. No. 1.5e+04;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 0 A; 12 C; 0 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Columns 17-18; 168pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PROF-) PROFILE DIAGNOSTIC SCI INC.
                                     bacteria; oncogene; virus; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
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Local Similarity 88.2%;
les 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-0173489.
92US-0968436.
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(first entry)
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The sequence is an antisense molecule directed against position -3 to +18, relative to the start codon of the gene for mouse fibroblast growth factor 1. The polynucleotide can be used for inhibiting vascular smooth muscle cell proliferation and for treating a disease e.g. vascular stenosis, post angioplasty restenosis, atherectomy, atherosclerosis, atrial venous shunt failure, cardiac hypertrophy, vascular surgery and organ transplant. See also AAQ70313-60. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is an antisense molecule directed against position -6 to +15, relative to the start codon of the gene for mouse fibroblast growth factor 1. The polynucleotide can be used for inhibiting vascular smooth muscle cell proliferation and for treating a disease e.g. vascular stenosis, post angioplasty restenosis, atherectomy, atherosclerosis, atrial venous shunt failure, cardiac
                                                                                                                                                                                                                                                                                                                                                                Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fibroblast growth factor; hybridisation; laser procedures; vascular smooth muscle cell; proliferation; SMC; vascular stenosis; post angioplasty restenosis; atherosclerosis; cardiac hypertrophy; organ transplant; ss.
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                                    growth
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                                                                                                                                                                                                                                                                                                                                             76.7%; Score 13.8; DB 15;
88.2%; Pred. No. 1.5e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New anti-sense polynucleotide(s) to fibroblast receptor - used for inhibiting vascular smooth proliferation, partic. for treating restenosis
                                  New anti-sense polynucleotide(s) to fibroblast receptor - used for inhibiting vascular smooth proliferation, partic. for treating restenosis
                                                                                                                                                                                                                                                                                                                            Sequence 21 BP; 4 A; 12 C; 2 G; 3 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense oligonucleotide for mouse FGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 9; 53pp; English.
                                                                                                         Claim 3; Page 9; 53pp; English
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Or
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AAQ70345 standard; DNA; 21
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-249123/30.
WPI; 1994-249123/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TEXA-) TEXAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
15-FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ70345;
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 76.7%; Score 13.8; DB 15; Length 18; Best Local Similarity 88.2%; Pred. No. 1.5e+04; Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fibroblast growth factor; hybridisation; laser procedures; vascular smooth muscle cell; proliferation; SMC; vascular stenosis; post angioplasty restenosis; atherosclerosis; cardiac hypertrophy; organ transplant; ss.
                                                                                                                                                                                                                                                                                        growth muscle
                                                                                                                                                                                                                                                                                     New anti-sense polynucleotide(s) to fibroblast receptor - used for inhibiting vascular smooth proliferation, partic. for treating restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 BP; 3 A; 11 C; 1 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dixon RA;
                                                                                                                                                                                                                 Dixon RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense oligonucleotide for mouse FGF
                                                                                                                                                                                                                  Rege AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dixon RAF, Rege AA,
                                                                                                                                                                             (TEXA-) TEXAS BIOTECHNOLOGY CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TEXA-) TEXAS BIOTECHNOLOGY CORP
                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 9; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGAGGGGGCTGGAA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВР.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 GGGATGTGGGGCTGGAA 2
                                                                                                       93WO-US12600
                                                                                                                                         92US-0999706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ70342 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (updated)
(first entry)
                                                                                                                                                                                                               Dixon RAF,
                                                                                                                                                                                                                                                 WPI; 1994-249123/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
15-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-DEC-1993;
                                                                                                    28-DEC-1993;
                                                                                                                                          31-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-DEC-1992;
                               WO9415945-A1
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                                                                   21-JUL-1994
                                                                                                                                                                                                               Denner LA,
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Synthetic.
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AAQ70342/ RESULT

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Denner

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Gaps

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BP; 2 A; 12 C; 2 G; 5 T; 0 other;

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Sequence 21
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                                                                                                                                                                                       RESULT 10
AAZ18648
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AAA93151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensics, paternity testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of the human gene SNPS shown in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism; pulmonary embolism; paternity test; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McCarthy JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and atherosclerosis -
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag= a
/standard_name= "single nucleotide polymorphism"
                                                                                                                                        .
0
                                                                                                  Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Daley GQ,
                                                                                                                                      Indels
 hypertrophy, vascular surgery and organ transplant.
                                                                                                  76.7%; Score 13.8; DB 15;
88.2%; Pred. No. 1.5e+04;
                                                                                                                                                                                                                                                                                                                                                                                                   Human gene single nucleotide polymorphism #1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bolk S,
                 See also AAQ70333-60.
(Updated on 25-MAR-2003 to correct PN field.)
                                                                 Sequence 21 BP; 4 A; 11 C; 2 G; 4 T; 0 other;
                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (WHED ) WHITEHEAD INST BIOMEDICAL RES (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ireland JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Examples; Page 145; 242pp; English.
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                                                                                                                                                                        2 GGGAGGGGGCTGGAA 18
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                                                                                                                                                                                                        N
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26-JUL-2000; 2000US-0220947.
16-AUG-2000; 2000US-0225724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-SEP-2000; 2000WO-US24503
                                                                                                                                                                                                      18 GGGATGTGGGGCTGGAA
                                                                                                                                                                                                                                                                           AAF96659/c
ID AAF96659 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                   Best Local Similarity 88.2
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gargill M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-226749/23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                   06-JUN-2001
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                                                                                                                                                                                                                                                                                                                               AAF96659
                                                                                                     Query Match
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                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASTH1; asthma; human; chromosome llp; ASTH11; ASTH1J; genetic locus; therapeutic; immunogen; polymorphism; junction; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                     Length
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalian asthma related genes, useful for diagnosis of predisposition to development of asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carey AH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 13.4; DB 20;
Pred. No. 2.1e+04;
0; Mismatches 1;
                   Score 13.8; DB 22;
Pred. No. 1.5e+04;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ASTH1 gene intron/exon junction sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cardon L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 57; 195pp; English
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Galvin M, Miller A, North M;
                                                                                                                 1 GGGGAGGAGGGCTGGA 17
                                                                                                                                                                                                                                                                                      ВР
                     76.7%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.4%;
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                                                                                                                                                                 21 GGGGAGGAGGCGCTGGA
                                                                                                                                                                                                                                                                                      AAZ18648 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Conservative
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AXYS-) AXYS PHARM INC.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-479058/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     19-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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ASTH1 locus, ASTH11; human; chromosome 11p; asthma; bronchial hyperreactivity; ets family; transcription factor; splice variant; genetic predisposition; polymorphism; antibody; drug screening; prophylaxis; therapy; diagnosis; exon boundary; ss.

Homo sapiens

US6087485-A. 11-JUL-2000

Human ASTH11 gene exon k 5' boundary region.

22-NOV-2000 (first entry)

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The present invention is concerned with a number of secreted proteins and their coding sequences isolated from various human cDNA libraries. The probes shown in the specification (AAA93132-A93156) can be used to obtain the cloned sequences from bacterial cells. The proteins and coding sequences can be used in the isolation of similar genes and proteins, in the elucidation of their function in vivo, and to treat a number of conditions. It is possible that they may have uses as nutritional supplements, as cytokine or cell proliferation factors, in immune modulation, where they may be used to treat immune and autoimmune diseases, as haematopoiesis regulators (treating myeloid or lymphoid cell deficiencies), in the promotion of tissue growth, they may have chemotical activity, haemostatic or thrombolytic activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New secreted proteins and polynucleotides encoding them, which are derived from Homo sapiens, useful for therapy, diagnosis, and research, as well as nutritional sources or supplements -
                                                                                                                   Human secreted protein; cytokine; cell proliferation;
nutritional supplement; immune modulation; autoimmune disorder;
haematopoiesis regulation; tissue growth; haemostasis; inflammation;
                                                                                         Clone vq15_1 secreted protein coding sequence probe SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rapiejko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hall J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 294; 309pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoffman H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or anti-inflammatory activity.
 ВР
                                                                                                                                                                                                                                                                                                                            99US-0120680.
99US-0298733.
99US-0149639.
99US-0155686.
99US-0157247.
99US-0167822.
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AAA93151 standard; DNA; 20
                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yuan O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ALPH-) ALPHAGENE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-549267/50.
                                                                                                                                                                                                                                   WO200049134-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Valenzuela D,
                                                                                                                                                                                                                                                                                                                              19-FEB-1999;
23-APR-1999;
17-AUG-1999;
23-SEP-1999;
01-OCT-1999;
                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                              15-FEB-2000;
                                                           12-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                               29-NOV-1999;
                                                                                                                                                                                                                                                                   24-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                            29-NOV-1999
                                                                                                                                                                         probe; ss.
                               AAA93151
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Cardon L, Buckler A;

Galvin M, Miller A, North M, Brooks-Wilson AR, Carey AH;

WPI; 2000-505109/45

(AXYS-) AXYS PHARM INC.

98US-0009913.

21-JAN-1998;

97US-0035663.

21-JAN-1997; 01-JUL-1997;

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XX

The invention relates to the ASTH1 locus on the short arm of human chromosome (11p). This locus comprises the ASTH11 and ASTH11 genes, which are associated with a genetic predisposition to asthma and bromons equence motifs. They are both expressed in opposite directions with the ASTH11 locus, and have similar patterns of expression and common sequence motifs. They are both expressed in creathea, lung and several other tissues. ASTH11 and ASTH13 are novel miplicated in the activation of a variety of genes including the TCRE implicated in the activation of a variety of genes including the TCRE of sehma. Both ASTH11 and ASTH13 men be important in the actiology of gene and cytokine genes known to be important in the actiology of attains of ASTH13, as the exons involved are all 5° to the start codon in carm of ASTH14, as the exons involved are all 5°, to the scaling contrast, alternative splicing of ASTH11 transcripts results of asth11 protein. The ASTH1 mucleic acids are useful as diagnostics to identify a hereditary predisposition to asthma, as probes for identifying expression of the gene in a biological specimen, and for generating genetically modified non-human animals or site specific gene modifications in cell lines. The encoded ASTH1 proteins are useful as immunogens to raise specific antibodies, in change screening for compositions that mimic or modulate activity or expression of ASTH1 and/or ASTH1 (including altered forms of these corrections, ASTH1 genomic regilatory regions, and anti-ASTH11 and creding are useful in the identification of individuals anti-ASTH11 and creding activity or expression of same activity or in vivo for prophylactic and therapeutic purposes. The interest ASTH11 or ASTH11 gene or active fragments therefor a ASTH11 gene or active fragments therefor a ASTH11 gene or boundary regions of the human ASTH11 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acids other than naturally occurring chromosomes encoding ASTH1 protein, for e.g. screening compositions that modulate expression or function of ASTH1 proteins or as diagnostics for genetic predisposition to asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.4%; Score 13.4; DB 21;
93.3%; Pred. No. 2.1e+04;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Examples; Column 37; 131pp; English.
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Best Local Similarity 93.3
Matches 14; Conservative
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1 GGGGAGGAGGGCTG 15

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AAA80555 standard; DNA; 20 BP.

RESULT 12 AAA80555

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AAA80555

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Gaps

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74.4%; Score 13.4; DB 21; Length 20; 93.3%; Pred. No. 2.1e+04; iive 0; Mismatches 1; Indels (

Conservative

Query Match Best Local Similarity Matches 14; Conserva'

Sequence 20 BP; 7 A; 1 C; 10 G; 2 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid molecule encoding human endothelin converting enzyme-3 protein, useful for screening modulators that are useful for treating atherosclerosis, myocardial and cerebral ischemia, and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                        hermorrhage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                       ECE-3; endothelin converting enzyme 3; hypertension; artherosclerosis; vascular restenosis; myocardial ischemia; cerebral vasospasm; subarachnoid hermorrh congestive heart failure; diabetes; endotoxic shock; migraine; Raynaud's disease; pulmonary disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 13; DB 21; Length 21; Pred. No. 3e+04; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 3 A; 3 C; 12 G; 3 T; 0 other;
                                                                                                               Primer #2 used to isolate human ECE-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 40; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Conservative 0;
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ABK00898 standard; RNA; 17 BP.
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                            AAC68417 standard; DNA; 21
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Human, ss, antisense therapy, cytostatic, antiinflammatory, haemostatic, cerebroprotective; nootropic, neuroprotective; antiparkinsonian, muscular, CD20, neurite growth inhibitor gene; NOGO, hammerhead ribozyme, DNAzyme; inozyme; G-cleaver, amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphoma; leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease;
                                                                                                                                             Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
                                                                                                                                                                                                                                                                                                                                                                                                     Chowrira BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and central nervous system injury
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28-FEB-2000; 2000US-185516P.
06-MAR-2000; 2000US-187128P.
                                                                                                                                                                                                                                                             09-FEB-2001; 2001WO-US04273
                                                                                                                                                                                                                                                                                                                                       (RIBO-) RIBOZYME PHARM: (BLAT/) BLATT L. (MCSW/) MCSWIGGEN J. (CHOW/) CHOWRIRA B M.
                                                                                                                                                                                                                                                                                                                                                                                                     McSwiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-607195/69
                                                                                                                                                                                                            WO200159103-A2.
                                                                                                                                                                        sapiens
                                                                                                                                                                                                                                    16-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                     Blatt L,
                                                                                                                                                                                    Synthetic
                                                                                                                                                                        Homo
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Claim 88; Page 80; 200pp; English.

The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neutric growth inhibitor gene (NOGO).

The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNAzyme) an Inozyme (an endolytic nucleic acids (e.g. a ribozyme or a DNAzyme) an Inozyme (an endolytic nucleic acids (e.g. a ribozyme or a DNAzyme) an Inozyme (an endolytic nucleic acid cleaving RNA with a NNN motif) pra an myerzyme (cleaving RNA with a NNN motif) pra an myerzyme (cleaving RNA with a NNN motif) prace control or cleaving RNA with a NNN motif) prace control or cleaving RNA with a NNN motif or cleaving RNA with a NNN motif or collaring a condition that is preferably Mg^2+. Furthermore, it may be contacted with a cell to reduce CC cleave RNA of CD20 in the presence of a divalent cation that is condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting customer or follicular NHL, lymphocytic leukaemia, B-call or collicular nucleic acid may be used to treat lymphoma, leukaemia, B-call or collicular nucleic acid may be used to later language or follicular nucleic acid may be contacted with a cell to reduce NOGO gene in the presence of a divalent cation that is preferably Mg^2+. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and divalent cation that is preferably Mg^2+. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and divalent cation that is preferably mylologate with the level of NOGO cativity of the central nervous system (NNS) injury and cerebrovascular accident (CVA, stroke), Alaheimer's disease, dementia, multiple sclerosis (Ms), chemotherapy-induced neuropathy, and/or other neurodegenerative disease disease, muscular disease, cataxia, Huntington's disease, creates which respond to the modulation of NOGO expression. The

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to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg^2. +. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting concleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky concleic acid may be used to treat lymphocytic lymphoma (NHL), bulky concleic acid is used to leave RNL, lymphocytic lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-targetting concleic acid is used to cleave RNA of the NOGO activity of the cell and thrombocytopaenia, and inflammatory arthropathy. The NOGO-targetting cation that is preferably Mg^2+. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of NOGO. The treat a patient having a condition associated with the revel contrains further comprise the use of one or more therapies.

CI n particular, the NOGO-targetting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, and/or tother neurodegenerative disease tisease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present sequence is an inozyme of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 71.1%; Score 12.8; DB 23; Length 17; Best Local Similarity 87.5%; Pred. No. 3.6e+04; Matches 14; Conservative 0; Mismatches 2; Indels C
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The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; MHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; cercopactive disease. Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
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                                                                                                            Length 17;
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                                                                                                    Query Match 71.1%; Score 12.8; DB 23; Best Local Similarity 87.5%; Pred. No. 3.6e+04; Matches 14; Conservative 0; Mismatches 2;
               present sequence is an inozyme of the invention.
                                                           Sequence 17 BP; 0 A; 13 C; 1 G; 3 U; 0 other;
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) BLATT L.
) MCSWIGGEN J.
) CHOWRIRA B M.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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1 (bases 1 to 16)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished
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or69hll.sl NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1601157 3'
similar to SW:PRPE HUMAN P02811 BASIC PROLINE-RICH PEPTIDE P-E
jcontains element MSR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                           from the Jackson
                                                                                                                                                                                                                                                                                                                         /sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jacksor
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      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource
                          Insert Length: 10000 Std Error:
Plate: 0010 row: L column: 24
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/64"
                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="UUGC1M0010L24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA968729.1 GI:3143909
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1. .16
/organism="HOMC ____
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1601157"
/tissue_type="pooled germ cell tumors"
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...red by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AU254493 3'-directed mouse cDNA library Mus musculus cDNA clone BED0002246 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

(bases 1 to 21)
Kato, K. and Matoba, R.
Generation of expressed sequence tags from mouse brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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/db_xref="taxon:10090"
/clone="BED0002246"
/tissue_type="brain"
/clone_lib="3'-directed mouse cDNA library"
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Graduate School of Biological Sciences
Graduate School of Biological Sciences
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkato@bs.aist-nara.ac.jp/BED/index.html.
URL:http://love2.aist-nara.ac.jp/BED/index.html.
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Trace considered overall poor quality
Insert Length: 514 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. ....
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/Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/Globe lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1M0358B07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0358B07 F, genomic survey sequence.
AZ512534

AZ512534.1 GI:10693850
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                            Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Pred. No. 1.3e+06;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0367 row: C column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0367C13"
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Mus musculus (house mouse)
Mus musculus
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1 Similarity 86.7%; Pro
13; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                              Rm. 308, B:
84112, USA
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2324392"
/tissue type="adenocarcinoma"
/lab_host="DH10B"
/clone lib="NCI_CGAP_Pan1"
/clone lib="NCI_CGAP_Pan1"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"
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20 bp DNA linear GSS 13-DEC-2000 1M0367C13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0367C13 F, genomic survey sequence.
AZ579495
AZ579495.1 GI:11693924
GSS
                                                                                                                                                                                                                   AI696833
wc74e09.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2324392 3'
similar to TR:01942 EXTENSIN ; contains element TAR1
repetitive element ;, mRNA sequence.
AI696833
AI696833.1 GI:4984733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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1 (bases 1 to 19)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished
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Mus musculus
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi;
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                 Gaps
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Pred. No. 1.3e+06;
); Mismatches 2; Indels
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               Mismatches
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Best Local Similarity 86.7%;
Matches 13; Conservative (
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Homo sapiens
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AZ579495
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Gaps

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REFERENCE AUTHORS

JOURNAL COMMENT

TITLE

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi #4732114 |gb |AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab host="E. Coli strain XLI0-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: PWD42nv; Purified genomic DNA from Musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
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Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genet
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Unpublished
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AZ493581/c
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                                                                                             REFERENCE
AUTHORS
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AZ345792
AZ345792.1 GI:10425029
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                                                                                                                                                                                                                                                                           Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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musculus C57BL/67 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606

Eax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0358 row: B column: 07

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Class: plasmid ends
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Matches 1
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source

FEATURES

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IS DNA linear GSS 05-OCT-2000 IM0328A24F Mouse 10kb plasmid UUGCIM library Mus musculus genomic close UUGCIM0328A24 F, genomic survey sequence.
AZ493581 AZ493581.1 GI:10667400 GSS 05-OCT-2000 GSS 05-OCT-200
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Score 11.4; DB 28; Length 19;
Pred. No. 1.7e+06;
0; Mismatches 1; Indels (
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VERSION
KEYWORDS
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Mus musculus (house mouse)

ACCESSION VERSION KEYWORDS SOURCE

LOCUS DEFINITION

RESULT 7 AZ345792

BASE COUNT ORIGIN

Ι'n

E., SLC,

SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL

TITLE

FEATURES

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http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 |gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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20 bp DNA linear GSS 14-DEC-2000
1M0510B10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0510B10 R, genomic survey sequence.
AZ645269
                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
84112, USA
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Location/Qualifiers
                                     Mus musculus (house mouse)
Mus musculus
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/clone lib="Mouse 10kb plasmid UUGC1M library"
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20 bp DNA linear GSS 05-OCT-2000 1M0357118R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0357118 R, genomic survey sequence.
AZ512326
AZ512326.1 GI:10693642
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Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mouse whole genome scaffolding with paired end reads from 10kb
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0328 row: A column: 24
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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81.2%;
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Best Local Similarity 81.2
Matches 13, Conservative
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84112, USA
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RESULT 9 AZ512326/c LOCUS

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ACCESSION VERSION

BASE COUNT ORIGIN

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ORGANISM

VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

JOURNAL COMMENT

TITLE

FEATURES

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was hydrodymanically sheared by repeated passage through a was hydrodymanically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0242012F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
                                                                              Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinse; I to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
'M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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84112, USA
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/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
                                AZ772707.1 GI:12896303
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Fax: 801 585 7177
Email: ddunn@genet
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1M0583L18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0583L18 R, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reiliy, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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/lab_host="E. Coli strain XLI0-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackso:
Laboratory Mouse DNA Resource
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0510 row: B column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
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                                                          Mus musculus (house mouse)
Mus musculus
AZ645269.1 GI:11774602
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RESULT 11 AZ772707/c LOCUS DEFINITION

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                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; Mammoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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clone UUGC2M0242012 F, genomic survey sequence.
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0242 row: O column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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University of Utah Genome Center
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                                                                                       Mus musculus (house mouse)
Mus musculus
                      AZ969440
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Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
1M0219P12R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0219P12 R, genomic survey sequence.
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Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Dm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Pred. No. 2e+06;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0219 row: P column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory Mouse DNA Resource
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/clone="UUGC1M0219P12"
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Location/Qualifiers
                                                                                                                                                                 Mus musculus (house mouse)
Mus musculus
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL COMMENT

TITLE

LOCUS DEFINITION

ACCESSION

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114 |gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                             AZ495585
1M0331H02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0331H02 R, genomic survey sequence.
                                                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
Mus musculus
Mus musculus

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, K., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

Dlasmid inserts

Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.2%; Score 11.2; DB 28; ilarity 81.2%; Pred. No. 2e+06; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 80 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0331 row: H column: 02
Seq primer: CACACAGGAAACAGCTATGACC
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High quality sequence stop: 21.
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|13; Conserva
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Best Local S:
Matches 13
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ORIGIN
                                                                                  DEFINITION
                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                            ACCESSION
VERSION
KEYWORDS
                         AZ495585/c
                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
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                           GSS 04-OCT-2000
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
21 bp DNA linear GSS 04-OCT-201
1M0295F12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0295F12 F, genomic survey sequence.
AZ476392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Outract: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Wiversity of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lob host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0295 row: F column: 12
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                                                                                                                                                                                                 Mus musculus (house mouse)
Mus musculus
                                                                                                                      AZ476392.1 GI:10634517
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGGGAGGAGGGCTGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Male"
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rm. 308, Bi
84112, USA
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ORIGIN
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FEATURES

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Gaps

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21 GGGGTGGGGGGGGGGG

RESULT 15

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Length 21; Indels

Search completed: October 27, 2003, 13:59:24 Job time: 1583.77 secs

Sequence 157, Appl Sequence 128, Appl Sequence 128, Appl Sequence 128, Appl Sequence 2, Appli Sequence 17, Appli Sequence 68, Appli Sequence 6, Appli

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; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; TITLE OF INVENTION: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
                                                                                                                                                                                                                                                     ALIGNMENTS
    Sequence 9, Appli
Sequence 21, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 21, Appli
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Sequence 10, Appl
Sequence 13, Appl
Sequence 298, App
Sequence 21, Appl
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              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-173-489C-128
PCT-US93-12600-11
PCT-US93-12600-11
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US-08-250-856A-21
US-08-456-905A-21
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US-08-37-120A-27
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                                                                                                                                                                                                                            569978 segs, 220691566 residues
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Maximum Match 100%
Listing first 45 summaries
                                                               nucleic search, using sw model
                                                                                                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                ggggaggagggctggaa 18
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                                                                                                                                     US-09-331-204A-5
18
1 ggggaggagggctg
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                                                                                                                                                                                                                                                                            length: 0
length: 22
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Match
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9
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Perfect score:
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Minimum DB Maximum DB

Database

Result

0 0 0 0

TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from alpha-1DESCRIPTION: globin sequence region in Seq ID No. 5861244127 USING DNA ဝ JOIN TO THE STATE OF THE STATE: NEW YORK S 128 : FROM 1 COUNTRY: USA
ZID: 10021.

COMPUTER READABLE FORM:
MEDIUW TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 2.DEC 1993
CLASSIFICATION AJS
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 2.9 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
RECISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: .. ON TYPE: nucleic acid STRANDEDNESS: single stranded SEQ ID ANTI-SENSE: no PUBLICATION: RELEVANT RESIDUES IN SI US-08-173-489C+128

Sequence 26, A Sequence 6, Ap Sequence 126,

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Sequence Sequence Sequence

Sequence 48 Sequence 49

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CLASSIFICATION:
PRIOR APPLICATION DATA:
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; Sequence 10, Application PC/TUS9312600
; GENERAL INFORMATION:
; APPLICANT: Denner, Larry A.
; APPLICANT: Rege, Ajay A.
; APPLICANT: Dixon, Richard A.F.
; TITLE OF INVENTION: ANTISENSE MOLECULES DIRECTED AGAINST A
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR RECEPTOR GENE FAMILY
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 18;
    Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 76.7%; Score 13.8; DB 5; Length 1 Best Local Similarity 88.2%; Pred. No. 1.4e+03; Matches 15; Conservative 0; Mismatches 2; Indels
Query Match 76.7%; Score 13.8; DB 2; Length 1 Best Local Similarity 88.2%; Pred. No. 1.4e+03; Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12600
FILING DATE: 28-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/999,706
FILING DATE: December 31, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GGGAGGAGGGCTGGAA 18
                                                                        1 GGGGAGGAGGGCTGGA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                         17 GGGGAGGAGGAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
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ADDRESSEN: Dressier, Goldmith, Shore & ADDRESSEN: Milanew, Ltd.

CTITY: Chicago: Milanew, Ltd.

CTITY: Chicago: Milanew, Ltd.

CTITY: Chicago: Milanew, Ltd.

CTITY: Chicago: Milanew, Ltd.

COMPUTER: 1100 No. 100 Milane

COMPUTER: Talk PC Compatible

COMPUTER: Talk PC COMPATIB
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RESULT 7
US-08-468-037A-9/c
US-08-468-037A-9/c
; Sequence 9, Application US/08468037A
; Patent No. 585921
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; APPLICANT: A. Kawasaki
; TITLE OF INVENTION: 2'-Modified Oligonucleotides
; UNMER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859221ris
; STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
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Sequence 21, Application US/08250856A
Featent No. 5563256
Featent No. 5563256
Featent No. 5563256
GENERAL INFORMATION:
APPLICANT: Wonia, Brett P. and Boggs, Russell T.
ITLE OF INVENTION: Of raf Gene Expression
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: Jol Lake Drive East, Suite 201
CITY: Cherry Hill
COUNTRY: USA
ZIP: 08002
COMPUTER: BEADELE FORM:
MEDIUM TYPE: DISKTTE, 3.5 INCH, 1.44 MD STORAGE
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: MORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,856A
FILING DATE: May 31, 1994
CLASSIFICATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: 32,257
REFERENCE/DOCKET NUMBER: 120-20-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.1%; Score 12.8; DB 1; Length 20; B7.5%; Pred. No. 3.7e+03;
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TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 21
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGGGAGGAGGGCTGG 16
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: Sir
STRANDEDNESS: Sir
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-08-250-856A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.7%; Score 13.8; DB 5; Length 21; 88.2%; Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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           US 07/999,706
APPLICATION NUMBER: US 07/999,
FILING DATE: December 31, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
TELEFAX: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GGGAGGAGGGCTGGAA 18
                                                                                                                                                                                                                                                                                                                                                              linear
E: DNA (genomic)
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 76.7
Best Local Similarity 88.2
Matches 15, Conservative
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US-09-009-913-298
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US-08-756-806A-21/C
; Sequence 21, Application US/08756806A
; Patent No. 595229
; GENERAL INFORMATION:
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation
; TITLE OF INVENTION: of raf Gene Expression
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; CORRESPENCE ADDRESS:
; STREET: 66 East Main Street
; CITY: Marlton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 20;
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ZIP: 08053

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/756,806A

FILING DATE: No. 5952229ember 26, 1996

CLASSIFICATION DATA:

APPLICATION NUMBER: PCT/US95/07111

FILING DATE: May 31, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/250,856

FILING DATE: May 31, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata

REGISTRATION NUMBER: ISPH-0200

TELECOMMUNICATION INFORMATION:

TELEPHONE: (600) 779-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 12.8; DB 2;
Pred. No. 3.7e+03;
0; Mismatches 2;
                                                                                                                                                                                                      Query Match 71.1%; Score 12.8; DB 2; Best Local Similarity 87.5%; Pred. No. 3.7e+03; Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 71.1%;
Best Local Similarity 87.5%;
Matches 14; Conservative
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
                                                                : TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
US-08-471-973A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acid
EDNESS: Single
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TI-SENSE: Yes
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Sequence 9, Application US/08471973A
Sequence 9, Application US/08471973A
Sequence 9, Application US/08471973A
Sequence 9, Application US/08471973A
GENERAL INFORMATION:
APPLICANT: Phillip Dan Cook
APPLICANT: Andrew Kawasaki
TITLE OF INVENTION: Sugar Modified Oligonucleotides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5872232ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 71.1%; Score 12.8; DB 2; Length 20; Best Local Similarity 87.5%; Pred. No. 3.7e+03; Matches 14; Conservative 0; Mismatches 2; Indels
   ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,037A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 835,932
FILING DATE: 05-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: JOSEPH LUCCI
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: 15IS-2004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NOWBER: 15IS-568-3100
TELECOMMUNICATION NOWBER: 15IS-568-3100
TELECOMMUNICATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
TWDE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,973A
FILING DATE: 06-JUN-1995
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 835,932
FILING DATE: 05-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: IS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGGAGGAGGGGCTGG 16
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20 bases
LYPE: nucleic acid
STRANDEDNESS: single
7 TOPOLOGY: linear
7 ANTI-SENSE: yes
US-08-468-037A-9
Query Mar
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COUNTRY: L
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Sequence 21, Application US/09143214

Patent No. 609626

GENERAL INFORMATION:
TITLE OF INVENTION: Antisense Oligonucleotide Modulation
TITLE OF INVENTION: of raf Gene Expression
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: NGS3
COUNTRY: USA
ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/143,214
FILING DATE:
CLASSIFICATION NUMBER: US/09/143,214
FILING DATE:
APPLICATION NUMBER: PCT/US95/07111
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07111
FILING DATE: May 31, 1995
APPLICATION NUMBER: 08/250,856
FILING DATE: May 31, 1994
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 71.1%; Score 12.8; DB 3; Best Local Similarity 87.5%; Pred. No. 3.7e+03; Matches 14; Conservative 0; Mismatches 2;
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035,357
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/468,037
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REGISTRATION NUMBER: ISIS-2004
TELEPHONE: 215-568-3439
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
TELEGISTICATION OF SEQ ID NO: 9:
LENGTH: 20 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISPH-0200
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REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: 1SPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 810-1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32,257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-09-143-214-21/c
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                                                                           Sequence 9, Application US/08465880
Patent No. 595589
GENERAL INFORMATION:
APPLICANT: Philip Dan Cook
TITLE OF INVENTION: Gapped 2' Modified Oligonucleotides
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5955589ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09035357

Sequence 9, Application US/09035357

GENERAL INFORMATION:

APPLICANT: Phillip Dan Cook
APPLICANT: A. Kawasaki
TITLE OF INVENTION: 2'-Modified Oligonucleotides
NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                           CITY: FILLENCE...

STATE: PA

COUNTRY: 0.S.A.

ZIE: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,880
FILING DATE: Herewith
CLASSIFICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 214,993
FILING DATE: 2.-JUN-1994
ATTORNEY/AGENT INFORMATION:
MAME: Joseph Lucci
REGISTRATION NUMBER: 1SIS-2002
TELEFAX: 215-568-3100
TELEFAX: 215-568-310
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS: LENGTH: 20 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MS-08-465-880-9
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Query Match 71.1%; Score 12.8; DB 4; Best Local Similarity 87.5%; Pred. No. 3.7e+03; Matches 14; Conservative 0; Mismatches 2;
                                                                                                    COMPUTER NEAR AND ALLE FORM;

COMPUTER: 1EM PC COMPATIBLE
COMPUTER: 1EM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,202
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION OBTA:
APPLICATION NUMBER: 08/471,973
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: JOSEPH LUCCI
REFERENCE/DOCKET NUMBER: 1SIS-2005
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: antisense sequence US-09-506-073-21
                                                                                                                                                                                                                                 US/09/135,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/09506073; Patent No. 6410518; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.18;
87.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGGAGGAGGAGCGGG 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 130
SEQ ID NO 21
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
EDNESS: single
                                                                                         COMPUTER READABLE FORM:
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Best Local Similarity
STATE: E... COUNTRY: U.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS
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OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: alternative oligonucleotide with uniform; OTHER INFORMATION: phosphorothiate backbone with nucleotides 10-20; OTHER INFORMATION: being substituted by methoxy at the 2' position of; OTHER INFORMATION: the sugar moiety
US-09-000-136-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/09135202
Patent No. 6399754
GENERAL INFORMATION:
APPLICANT: Phillip Dan Cook
APPLICANT: Andrew Kawasaki
TITLE OF INVENTION: Sugar Modified Oligonucleotides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6399754ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09000136

Sequence 7, Application US/09000136

Patent No. 6096720

GENERAL INFORMATION:

APPLICANT: Love, William G

APPLICANT: Sharman, Thomas

APPLICANT: Phillips, Judith A

APPLICANT: Nicklin, Paul L

APPLICANT: Nicklin, Paul L

APPLICANT: Nicklin, Raren O

TITLE OF INVENTION: Liposomal Oligonucleotide Compositions

FILE REFERENCE: 4-20536/A/MA 2112

CURRENT APPLICATION NUMBER: US/09/000,136

CURRENT FILING DATE: 1998-04-23

EARLIER PILING DATE: 1995-08-01

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NIMMER OF CEO TE MOSC. 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 71.1%; Score 12.8; DB 3; Length 20; Best Local Similarity 87.5%; Pred. No. 3.7e+03; Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                   Length 20;
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                 Query Match 71.1%; Score 12.8; DB 3; Best Local Similarity 87.5%; Pred. No. 3.7e+03; Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: phosphorothioate backbone FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGGAGGAGGGCTGG 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 GGGGAGGAGGAGCGGG
             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
                                                                                                                Single
                                                                                       Nucleic Acid
                                                                                                          ; STRANDEDNESS: Sin
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-09-143-214-21
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-000-136-7/c
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Gaps

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Length 20; Indels

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APPLICANT: Monia, Brett P.

ATTLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/506,073
CURRENT FILING DATE: 2000-02-18
EARLIER APPLICATION NUMBER: WS 09/143,214
EARLIER APPLICATION NUMBER: PCT/US98/13961
EARLIER FILING DATE: 1998-07-06
EARLIER APPLICATION NUMBER: US 08/888,982
EARLIER PILING DATE: 1998-07-06
EARLIER APPLICATION NUMBER: US 08/756,806
EARLIER PILING DATE: 1996-11-26
EARLIER PILING DATE: 1996-11-26
EARLIER FILING DATE: 1996-05-31
EARLIER FILING DATE: 1995-05-31
EARLIER FILING DATE: 1994-05-31
EARLIER FILING DATE: 1994-05-31
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ò Dp Search completed: October 27, 2003, 14:03:34 Job time: 42.3143 secs

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October 27, 2003, 11:25:34; Search time 387.943 Seconds (without alignments) 124.432 Million cell updates/sec
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cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

cgn2_6/ptodata/1/pubpna/DSC6_NEW PUB.seq:*

cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

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cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1792395 seqs, 1340900451 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTITY NUC Gapoxt 1.0
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18
1 9999a9999ct99aa 18
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                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Sequence 7484, Ap	Sequence 7485, Ap	Sequence 898, App	668	Sequence 45, Appl	6	ດ	27,	Sequence 21, Appl	7486,	Sequence 7487, Ap	Sequence 1931, Ap	Sequence 1932, Ap	Sequence 1933, Ap	Sequence 1934, Ap	Sequence 2409, Ap
SUMMARIES	ID	US-09-866-108-7484	US-09-866-108-7485	US-09-780-533A-898	US-09-780-533A-899	US-10-133-779-45	US-09-996-263-9	US-10-352-586-9	US-10-057-550-21	US-10-173-225B-21	US-09-866-108-7486	US-09-866-108-7487	US-10-061-201-1931	US-10-061-201-1932	US-10-061-201-1933	US-10-061-201-1934	US-09-780-533A-2409
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	Query Match Length DB	17	17	17	17	17	20	20	20	20	17	17	17	17	17	17	17
₩	Query Match	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1	68.8	68.8	68.9	68.8	68.8	68.8	67.8
	Score	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.4	12.4	12.4	12.4	12.4	12.4	12.2
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Sequence 46, Appl Sequence 47, Appl Sequence 900, App Sequence 1936, App Sequence 12, Appl Sequence 14, Appl Sequence 11, Appl Sequence 8084, App Sequence 8086, App Sequence 8086, App Sequence 349, App Sequence 340, App Sequence 341, App	equence 922 equence 923 equence 11, equence 5, equence 5, equence 6, equence 6, equence 6,
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ALIGNMENTS

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BASEULT 1

US-09-666-108-7484

) Sequence 7484, Application US/09866108

) Patent No. USZOO20048800A1

GENERAL IMPORMATION:

APPLICANT: UV. YIZhong

APPLICANT: UV. YIZhong

APPLICANT: HANZEL DAVIG R.

APPLICANT: SHAMNON MARK

TITLE REFERENCE: ADOULD-10 SOO 966,108

CURRENT APPLICANTION NUMBER: US/09/866,108

CURRENT APPLICANTION NUMBER: US/09/866,108

CURRENT APPLICANTION NUMBER: US/00/0666

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30
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Indels

Length 17;

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APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Chowrira, Bharat
APPLICANT: Chowrira, Bharat
APPLICANT: Haeberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBHB00,878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT APPLICATION NUMBER: US 60/181,797
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: Patentin version 3.0
SEQ ID NO 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 71.1%; Score 12.8; DB 11; Best Local Similarity 87.5%; Pred. No. 2.5e+04; Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                             Query Match 71.1%; Score 12.8; DB 9; Best Local Similarity 87.5%; Pred. No. 2.5e+04; Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
US-09-780-533A-898/c
; Sequence 898, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 6679
SOFTWARE: Patentin version 3.0
SEQ ID NO 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.18;
87.58;
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; ORGANISM: Homo sapiens
US-09-780-533A-899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA
CORGANISM: Homo sapiens
US-09-780-533A-898
     ; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7485
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .09-780-533A-899/c
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APPLICANT: RANK, DAVIG R.
APPLICANT: RANK, Weansheng
APPLICANT: CHEN, Weansheng
APPLICANT: STANKN, MAYE
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
CURRENT APPLICATION: WYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
CURRENT APPLICATION NUMBER: US/09/66,108
CURRENT FILING DATE: 2000-05-26
CURRENT FILING DATE: 2000-05-36
RRIOR APPLICATION NUMBER: US 60/236,359
RRIOR APPLICATION NUMBER: US 60/236,359
RRIOR APPLICATION NUMBER: US 60/236,359
RRIOR FILING DATE: 2000-01-30
RRIOR APPLICATION NUMBER: PCT/US01/0066
RRIOR FILING DATE: 2001-01-30
RRIOR PRILING DATE: 2001-01-30
RRIOR APPLICATION NUMBER: PCT/US01/00665
RRIOR APPLICATION NUMBER: PCT/US01/00665
RRIOR APPLICATION NUMBER: PCT/US01/00665
RRIOR APPLICATION NUMBER: PCT/US01/00666
RRIOR APPLICATION NUMBER: PCT/US01/00667
RRIOR FILING DATE: 2001-01-30
RRIOR APPLICATION NUMBER: PCT/US01/00667
RRIOR FILING DATE: 2001-01-30
RRIOR FILING DATE: 2001-01-30
RRIOR APPLICATION NUMBER: PCT/US01/00667
RRIOR FILING DATE: 2001-01-30
RRIOR RRIUM DATE: 2001-01-30
RRIOR R
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Pred. No. 2.5e+04;
0; Mismatches 2; Indels
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine; SEQ ID NO 7484
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7485, Application US/09866108 Patent No. US20020048800A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 71.1%; Sc
Best Local Similarity 87.5%; Pr
Matches 14; Conservative 0;
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JI, Yonggang
PENN, Sharron G.
HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7484
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Indels

Length 17;

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Sequence 899, Application US/09780533A;
Publication No. US20030060611A1;
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: Chowrira, Bharat
APPLICANT: Haeberli, Pere
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBHB00,878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/181,797
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US-10-057-550-21/C
US-10-057-550-21/C
Sequence 21, Application US/10057550
Fublication No. US20030032607A1
GENERAL INFORMATION:
TILLE REFERENCE:
TILLE REFERENCE:
FURENT APPLICATION NUMBER: US/10/057,550
CURRENT FILING DATE: 2002-01-25
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-09-06
PRIOR FILING DATE: 1998-09-06
PRIOR FILING DATE: 1998-09-06
PRIOR FILING DATE: 1998-07-06
PRIOR FILING DATE: 1998-07-06
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-01-26
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Sequence 9, Application US/10352586

Publication No. US20030187240A1

GENERAL INFORMATION:

APPLICANT: Cook, Phillip Dan

TITLE OF INVENTION: 2. -Modified Oligonucleotides

FILE REFERENCE: ISIS5137

CURRENT FILING DATE: 2003-01-28

PRIOR APPLICATION NUMBER: 09/389,283

PRIOR FILING DATE: 1999-09-02

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PatentIn Version 3.2
                                                                                                                                                                                                                                                                             Query Match 71.1%; Score 12.8; DB 11; Best Local Similarity 87.5%; Pred. No. 2.4e+04; Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 71.1%; Score 12.8; DB 12; Best Local Similarity 87.5%; Pred. No. 2.4e+04; Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                   ANTI-SENSE: yes
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Synthetic construct
US-10-352-586-9
                     TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                             1 GGGGAGGAGGGCTGG 16
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Sequence 9, Application US/09996263
Publication No. US20030004325A1
GENERAL INFORMATION:
APPLICANT: Phillip Dan Cook
Andrew Kawasaki
TITLE OF INVENTION: Sugar Modified Oligonuclectides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030004325A1ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
 Gaps
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                                                                                                                                                                                                     Sequence 45, Application US/10133779
Publication No. US20030165884A1
GENERAL INFORMATION:
APPLICANT: Chow, Robert
APPLICANT: Tonai, Richard
APPLICANT: Stemcyte, Inc.
TITLE OF INVENTION: High Throughput Methods of HLA Typing
FILE REFERENCE: 020035-000210US
CURRENT APPLICATION NUMBER: US/10/133,779
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: US/09/747,391
PRIOR FILING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 278
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 278
 Indels
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MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/996,263
FILING DATE: 28-NO. US20030004325A1-2001
CLASSIFICATION: AURKNOWN>
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REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-2005
TELECOMMUNICATION INFORMATION:
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/471,973
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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                                            1 GGGGAGGAGGGGCTGG 16
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                                                                                        GGGGAGGAGGGGAGG 1
14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CORGANISM: Homo sapiens
US-10-133-779-45
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Matches
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APPLICANT: GHEN, MAYLE K.
APPLICANT: GHEN, MAYLE K.
APPLICANT: GHEN, MAYLE K.
APPLICANT: GHENNOM MARK
TITLE OF INVENTION: MAYCSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
CURRENT PEDLICATION NUMBER: US/09/86,108
CURRENT FILING DATE: 2001-05-25
PRIOR FULING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-27
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-
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GENERAL INFORMATION:

APPLICANT: GU, Yizhong

APPLICANT: PENN, Sharron G.

APPLICANT: PENN, Sharron G.

APPLICANT: RANK, David K.

APPLICANT: RANK, David R.

APPLICANT: CHEN, Wensheng

APPLICANT: SHANNON, Mark

ITILE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: GB 24263.6
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Pred. No. 3.7e+04;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7487, Application US/09866108 Patent No. US20020048800A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 92.9%;
Matches 13; Conservative (
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US-09-866-108-7486
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US-10-173-225B-21/C

J Sequence 21, Application US/1017325B

Sequence 21, Application US/1017325B

Publication No. US20030119769A1

GENERAL INFORMATION: Breat P.

TILE OF INVENTION: Antiense Oligonucleotide Modulation of raf Gene Expression

FILE REFERENCE: ISPH-0665

CURRENT PFLICATION NUMBER: US/10/173,225B

CURRENT PILING DATE: 2002-01-25

PRIOR PAPLICATION NUMBER: US 09/143,214

PRIOR PELING DATE: 1998-07-07

PRIOR PELING DATE: 1996-07-07

PRIOR PELING DATE: 1996-07-07
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PRIOR APPLICATION NUMBER: PCT/US95/07111
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/250,856
PRIOR FILING DATE: 1994-05-31
NUMBER OF SEQ ID NOS: 130
SEQ ID NO 21
LENGTH: 20
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; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-173-225B-21
                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: antisense sequence US-10-057-550-21
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US-09-866-108-7486; Sequence 7486; Application US/09866108; Patent No. US20020048800A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: artificial sequence
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APPLICANT: GU, Yizhong APPLICANT: JI, Yonggang APPLICANT: PENN, Sharron G. APPLICANT: HANZEL, David K.

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                                                                                                                                                                                                                                                                                                                                                                   Score 12.4; DB 12;
Pred. No. 3.7e+04;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1932, Application US/10061201

Publication No. US20030166229A1

GENERAL INFORMATION:
HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PB0178

CURRENT FILING DATE: 2002-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PRIOR PRIOR DATE: 2001-01-30
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TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PB0178
                           PRIOR FILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 4162
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 1931
LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 92.9%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGGGAGGAGGGGT 14
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Matches 13, Conservative
                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-10-061-201-1931
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US-10-061-201-1932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-10-061-201-1932/c
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Pred. No. 3.7e+04;
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Publication No. US20030166229A1

GENERAL INFORMATION:

APPLICANT: Shannon, Mark

ITILE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1

FILE REFERENCE: PB0178

CURRENT PILING DATE: 2002-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR PILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
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92.9%;
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Best Local Similarity 92.9
Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108-7487
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Pred. No. 3.7e+04;
0; Mismatches 1;
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Sequence 1934, Application US/10061201
PUBLICATION NO. US20030166229A1
GENERAL INFORMATION:
APPLICANT: Shannon, Mark
TITLE OF INVENTION: HUWAN POSH-LIKE PROTEIN I
FILE REFERENCE: P80178
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 200
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
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Best Local Similarity 92.9%;
Matches 13; Conservative C
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US-10-061-201-1933
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Sequence 2, Appli
Sequence 5, Appli
Sequence 20, Appl
Sequence 60578, A
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1/pna/US6020 COMB.seq:*
1/pna/US6021 COMB.seq:*
1/pna/US6022 COMB.seq:*
1/pna/US6022 COMB.seq:*
1/pna/US6023 COMB.seq:*
1/pna/US6024 COMB.seq:*
1/pna/US6025 COMB.seq:*
1/pna/US6025 COMB.seq:*
1/pna/US6025 COMB.seq:*
1/pna/US6025 COMB.seq:*
1/pna/US6025 COMB.seq:*
1/pna/US6031 COMB.seq:*
1/pna/US6032 COMB.seq:*
a/l/pna/US6032 COMB.seq:*
a/l/pna/US6034 COMB.seq:*
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US-09-331-204A-5
US-09-331-204A-20
US-10-310-188-60578
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/pna/US6013_(
/pna/US6014_(
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/pna/US6016_
/pna/US6017_
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Match
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No.
                                                                                                                                                          ; Search time 2356.29 Seconds (without alignments) 253.343 Million cell updates/sec
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cgn2_6/ptodata/1/pna/USO6_COMB.seq:*
cgn2_6/ptodata/1/pna/USO6_COMB.seq:*
cgn2_6/ptodata/1/pna/USO8_COMB.seq:*
cgn2_6/ptodata/1/pna/USO81_COMB.seq:*
cgn2_6/ptodata/1/pna/USO81_COMB.seq:*
cgn2_6/ptodata/1/pna/USO81_COMB.seq:*
cgn2_6/ptodata/1/pna/USO83_COMB.seq:*
cgn2_6/ptodata/1/pna/USO93_COMB.seq:*
cgn2_6/ptodata/1/pna/USO93_COMB.seq
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                       nucleic search, using sw model
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Maximum Match 100%
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18
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Perfect score:
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Mismatches

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18; Conservative

Matches

e 5895, Ap e 5892, Ap e 61140, Ap e 64132, Ap e 64132, Ap e 61140, Ap e 61084, Ap e 61089, Ap e 1819, Ap e 1810, Ap e 1801, Ap e	Na o
Sequence 386 Sequence 6119 Sequence 61119 Sequence 61119 Sequence 6119 Sequence 6119 Sequence 6119 Sequence 111, Sequence 112, Sequence 113, Sequence 113, Sequence 113, Sequence 114 Sequence 115 Sequence 115 Sequence 116 Sequence 117 Sequence 118	MODULATING An oligomer kyribonuclei onsisting of intersugar intersugar
303-778-3565 310-188-5892 227-565-61140 227-565-61140 3310-188-84932 3310-188-61044 3310-188-61044 3310-188-61084 3310-188-61084 3310-188-41819 3310-188-41819 3310-188-41819 3310-188-41819 3310-188-41819 3310-188-41819 3310-188-41819 3310-188-41819 3310-188-41819 3310-188-41819 3310-188-41819 3310-188-41819 3310-188-41819 3310-188-41819 3310-188-41819 3310-188-1819 3310-188-1819 3310-188-1819 3310-188-1819 3310-188-1819 3310-188-1819 3310-188-1819 3310-188-1819 3310-188-1819 3310-188-1819 3310-188-1819 3310-188-18139 3310-188-18139 3310-188-18139 3310-188-18091	AMERS AND METHODS ,204 3927 tificial Sequence: onucleic acid or of includes oligomers ng bases, sugars and bases, sugars
50 US-10-303-778 50 US-10-310-189 50 US-10-310-189 50 US-10-310-188 50 US-10-303-778 50 US-10-310-188 50 US-10-303-778 50 US-10-310-188	133120 OLIGO 0LIGO 105/09 0CT/US 19 101 100 0100 01000 0100
44444444444444444444444444444444444444	ert G-RICE G-RICE IMMUNS Sequen NUMBER: 1997-1; 6 6 Ver. 2 Ver. 2 Ver. 2 Ver. 2 Teque Teq Teque Teque Teq Teque Teq Teq Teq Teq Teq Teq Teq Teq Teq Te
444444444444444 8888888888888888888888	-2 Applicati ORMATION: Tam, Rob NVENTION: NVENTION: ENCE: ICN ELICATION PLICATION PATER ATTITUT ATTITUT ORMATION: ORMATION: ORMATION: ORMATION:
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RESULT 2
US-09-331-204A-5

US-09-331-204A-5

Sequence 5, Application US/09331204A

Sequence 5, Application US/09331204A

GENERAL INFORMATION:

APPLICANT: ITON Pharmaceuticals, Inc.

APPLICANT: Tam, Robert

ITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Resp.

FILE REPRENCE: 216/013-0181

FILE REPRENCE: 216/013-0181

FILE REPRENCE: 1999-08-20

PRIOR APPLICATION NUMBER: PCT/US97/23927

PRIOR APPLICATION NUMBER: PCT/US97/23927

PRIOR FILING DATE: 1997-08-20

SOFTWARE: Patentin version 3.0

SEQ ID NO 5

LENGTH: 18

LENGTH: 18
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US-09-331-204A-20/c
US-09-331-204A-20/c
Sequence 20, Application US/09331204A
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Resp.
FILE REFERENCE: 216/013-0181
CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT FILING DATE: 1999-08-20
FRIOR APPLICATION NUMBER: PCT/US97/23927
FRIOR APPLICATION NUMBER: PCT/US97/23927
FRIOR PILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
LENGTH: 18
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US-10-310-188-60578

j Sequence 60578, Application US/10310188

j GENERAL INFORMATION:

j APPLICANT: ROSECTAGEMONICS

j TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN

j TITLE OF INVENTION: USES THEREOF

j FILE REFERENCE: 47487
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100.0%; Score 18; DB 19;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 0;
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; iOCATION: (5963161)...(5963177)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 6548
US-10-227-565-61140
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US-10-310-188-84932
; Sequence 84932, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGemonics
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION: US/10/310,188
; CURRENT APPLICATION DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 84932
LENGTH: 17
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                                     Sequence 61140, Application PC/TUS0225943
Sequence 61140, Application PC/TUS0225943
GENERAL INFORMATION.
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/US02/25943
CURRENT FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 64158
SOFTWARE: Proprietary
SEQ ID NO 61140
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 61140, Application US/10227565
Sequence 61140, Application US/10227565
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/227,565
CURRENT FILING DATE: 2002-08-26
SOFTWARE: Proprietary
SEQ ID NO 61140
LENGTH: 17
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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Pred. No. 8.9e+04;
0; Mismatches 1;
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; OTHER INFORMATION: Chromosome = 1
PCT-US02-25943-61140
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Best Local Similarity 93.8%; Pr
Matches 15; Conservative 0;
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es 15; Conservative
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US-10-227-565-61140/c
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
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US-10-303-778-3565/c
; Sequence 3565, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: ROSettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL;
; TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: Patentin version 3.1
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Pred. No. 3.6e+04;
0; Mismatches 1;
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Pred. No. 8.9e+04;
0; Mismatches 1;
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 60578
LENGTH: 22
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US-10-310-188-5892/c
; Sequence 5892, Application US/10310188
; GENERAL INFORMATION:
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93.8%;
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Best Local Similarity 94.1%;
Matches 16; Conservative (
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Best Local Similarity 33.2
Best Local Similarity 52.2
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Best Local Similarity 93.8
Matches 15; Conservative
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CRGANISM: Homo sapiens
US-10-310-188-60578
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US-10-303-778-3565
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LENGTH: 16
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LENGTH: 16
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RESULT 13
US-10-310-188-61084

i Sequence 61084, Application US/10310188

i Sequence 61084, Application US/10310188

i GENERAL INFORMATION:

APPLICANT: ROSELtaGemonics

TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENTITLE OF INVENTION: USES THEREOF

FILE REFERENCE: 47487

CURRENT APPLICATION NUMBER: US/10/310,188

CURRENT PILING DATE: 2002-12-19

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: PatentIn version 3.1

SEQ ID NO 61084

LENGTH: 18
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GENERAL INFORMATION:
APPLICANT: RosettaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENTITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 61077
LENGTH: 18
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Pred. No. 8.9e+04;
); Mismatches 1;
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Pred, No. 8.9e+04;
0; Mismatches 1;
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Best Local Similarity 93.8%;
Matches 15; Conservative (
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Best Local Similarity 93.8%;
Matches 15; Conservative
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CORGANISM: Homo sapiens
US-10-310-188-61077
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US-10-310-188-41819
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GENERAL INFORMATION:
APPLICANT: RosettaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENETILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 24767
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; Sequence 61140, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 61140
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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Pred. No. 8.9e+04;
0; Mismatches 1;
                                                                          Query Match 80.0%; Score 14.4; DB 50; Best Local Similarity 93.8%; Pred. No. 8.9e+04; Matches 15; Conservative 0; Mismatches 1;
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Pred. No. 8.9e+04;
0; Mismatches 1;
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APPLICANT: RosettaGemonics
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; LOCATION: (5963161)...(5963177)
; OTHER INFORMATION: Chromosome = 1
US-10-367-832A-61140
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93.8%;
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Best Local Similarity 93.8%;
Matches 15; Conservative (
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Best Local Similarity 93.8'
Matches 15, Conservative
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US-10-310-188-24767
            ; ORGANISM: Homo sapiens
US-10-310-188-84932
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US-10-310-188-61077
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RESULT 15
US-10-310-188-41829
Sequence 41829, Application US/10310188
GENERAL INFORMATION:
APPLICANT: ROSELTAGEMONICS
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PALENTIN Version 3.1
SEQ ID NO 41829
LENGTH: 21
TYPE: DNA
CORGANISM: Homo sapiens
US-10-310-188-41829
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Sequence 60578, Ap Sequence 84932, Ap Sequence 24767, A Sequence 61084, A Sequence 61084, A Sequence 41819, A Sequence 18119, A Sequence 18119, A Sequence 1829, A Sequence 5724, Ap Sequence 60062, A Sequence 60062, A Sequence 60062, A Sequence 61728, A Sequence 61728, A Sequence 59439, Ap Sequence 5944, A Sequence 5129, A Sequence 6129, A Seque
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                                                                                                                                                October 27, 2003, 11:09:34; Search time 307.029 Seconds (without alignments) 97.777 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pna/PCT NEW COMB.seq:*

2: /cgn2_6/ptodata/1/pna/US06 NEW COMB.seq:*

3: /cgn2_6/ptodata/1/pna/US07 NEW COMB.seq:*

4: /cgn2_6/ptodata/1/pna/US08 NEW COMB.seq:*

5: /cgn2_6/ptodata/1/pna/US09 NEW COMB.seq:*

6: /cgn2_6/ptodata/1/pna/US10 NEW COMB.seq:*

7: /cgn2_6/ptodata/1/pna/US10 NEW COMB.seq:*

7: /cgn2_6/ptodata/1/pna/US10 NEW COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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PCT-US02-38216-84932
PCT-US02-38216-84932
PCT-US02-38216-61084
PCT-US02-38216-61084
PCT-US02-38216-41829
PCT-US02-38216-41829
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PCT-US02-38216-61129
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match Length
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Maximum DB seq length: 22
                                                                                                                                                                                                                                                                     Title:
Perfect score:
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                                                                                                       OM nucleic
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No.
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Sequence 60580, A Sequence 10450, A Sequence 10450, A Sequence 6031, App Sequence 6031, App Sequence 6352, App Sequence 39123, App Sequence 39123, App Sequence 39123, App Sequence 42189, App Sequence 42189, App Sequence 60897, App Manual Ma		GROUP OF NOVEL VIRAL REGULATORY	Length 22; Indels 0; Gaps 0;		GROUP OF NOVEL VIRAL REGULATORY	Length 16; Indels 0; Gaps 0;
20 1 PCT-USO2-38216-60580 22 1 PCT-USO2-38216-10450 17 1 PCT-USO2-38216-5934 17 6 US-10-271-602B-105 18 1 PCT-USO2-38216-6031 18 1 PCT-USO2-38216-6080 18 1 PCT-USO2-38216-6445 18 1 PCT-USO2-38216-6445 19 1 PCT-USO2-38216-6445 19 1 PCT-USO2-38216-39006 19 1 PCT-USO2-38216-39006 19 1 PCT-USO2-38216-41632 19 1 PCT-USO2-38216-41632 19 1 PCT-USO2-38216-41632 19 1 PCT-USO2-38216-41632 19 1 PCT-USO2-38216-41632 19 1 PCT-USO2-38216-4189 20 1 PCT-USO2-38216-50897 20 1 PCT-USO2-38216-60897 20 1 PCT-USO2-38216-61897	ALIGNMENTS	tion PC/TUS0238216 DMICS LTD DINFORMATICALLY DETECTABLE BNES AND USES THEREOF ABER: PCT/US02/38216 2002-11-12 sion 3.2	85.6%; Score 15.4; DB 1; 94.1%; Pred. No. 4.4e+03; tive 0; Mismatches 1;	GCTGGA 17 GCTGGA 17	STECTABLE REOF 216	80.0%; Score 14.4; DB 1; 93.8%; Pred. No. 1.1e+04; Live 0; Mismatches 1;
27 13 72.2 29 12.8 71.1 30 12.8 71.1 32 12.8 71.1 34 12.8 71.1 35 12.8 71.1 36 12.8 71.1 37 12.8 71.1 39 12.8 71.1 40 12.8 71.1 41 12.8 71.1 42 12.8 71.1 43 12.8 71.1 44 12.8 71.1		T 1 S02-38216-60578 Uence 60578, Appl ERAL INFORMATION; FILCANT: ROSELTON; TLE OF INVENTION; TLE OF INVENTION; LE REFERENCE: 55C RRENT APPLICATION RRENT APPLICATION RRENT FILING DATE MBER OF SEQ ID NC FTWARE: Patentin ID NO 60578 ENGTH: 22 YPE: DNA RGANISM: HOMO Sal RGANISM: HOMO Sal	Query Match Best Local Similarity Matches 16; Conserva	1 GGGGAGGAGGGG 	RESULT 2 PCT-USO2-38216-5892/C Sequence 5892, Application PC/TUSO238216 GENERAL INFORMATION: GENERAL INFORMATION: TITLE OF INVENTION: GENES AND USES THEF TITLE OF INVENTION: GENES AND USES THEF FILE REFERENCE: 55002 CURRENT APPLICATION NUMBER: PCT/USO2/382; CURRENT FILING DATE: 2002-11-12 NUMBER OF SEQ ID NOS: 86841 SOFTWARE: PatentIn version 3.2 SEQ ID NO 5892 LENGTH: 16 TYPE: DNA ORGANISM: Homo sapiens PCT-USO2-38216-5892	Nuery Match Sest Local Similarity Fatches 15; Conserva
0 0000 0		SESCHOLL SECTION SECTI	ÓM Š	S G	MAN CANADA CANAD	- <u></u>

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Sequence 61084, Application PC/TUS0238216

Sequence 61084, Application PC/TUS0238216

GENERAL INFORMATION:

APPLICANT: ROSetta Genomics LTD

TITLE OF INVENTION: GENES AND USES THEREOF

FILE REFERENCE: 55002

CURRENT FILING DATE: 2002-11-12

CURRENT FILING DATE: 2002-11-12

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: Patentin version 3.2

SEQ ID NO 61084

LENGTH: 18
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SOFTWARE: A1819
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                                                                                       Length 18;
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                                                                                     Query Match 80.0%; Score 14.4; DB 1; Best Local Similarity 93.8%; Pred. No. 1.1e+04; Matches 15; Conservative 0; Mismatches 1;
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80.0%; Score 14.4; DB 1;

Best Local Similarity 93.8%; Pred. No. 1e+04;

Matches 15; Conservative 0; Mismatches 1;
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Best Local Similarity 93.8
Matches 15; Conservative
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; ORGANISM: Homo sapiens
PCT-US02-38216-41819
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CORGANISM: Homo sapiens
PCT-US02-38216-61084
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-61077
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PCT-US02-38216-41829
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                                                                                                                                  Sequence 84932, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 84932
LENGTH: 17
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Sequence 24767, Application PC/TUS0238216

GENERAL INFORMATION:

APPLICANT: ROSetta Genomics LTD

TITLE OF INVENTION: GENES AND USES THEREOF

FILE REFERENCE: 55002

CURRENT APPLICATION NUMBER: PCT/US02/38216

CURRENT FILING DATE: 2002-11-12

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: Patentin version 3.2
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APPLICANT: Rosetta Genomics LTD; TITLE OF INVENTION: GENES AND USES THEREOF; TITLE OF INVENTION: GENES AND USES THEREOF; FILE REFERENCE: 55002; CURRENT APPLICATION NUMBER: PCT/US02/38216; CURRENT FILING DATE: 2002-11-12; NUMBER OF SEQ ID NOS: 86841; SOFTWARE: Patentin version 3.2; SEQ ID NO 61077; LENGTH: 18
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   GGAGGAGGGCTGGAA 18
                                           16 GGAGGAGGGCTGGCA 1
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Best Local Similarity 93.8
Matches. 15, Conservative
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CORGANISM: Homo sapiens
PCT-US02-38216-24767
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Best Local Similarity
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LENGTH: 18
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ò g Sequence 41829, Application PC/TUS0238216 GENERAL INFORMATION: APPLICANT: Rosetta Genomics LTD TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY

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Sequence 18119, Application PC/TUS0238216
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
CURRENT FILING DATE: 2002-11-12
SOFTWARE: Patentin version 3.2
SEQ ID NO 18119
LENGTH: 20
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PCT-US02-38216-39028
; Sequence 39028, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT PILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 39028
; LENGTH: 21
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; GENERAL INFORMATION:
; APPLICANT: ROSELTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE PERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PATENTIN VERSION 3.2
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CRGANISM: Homo sapiens
PCT-US02-38216-18209
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ORGANISM: Homo sapiens
PCT-US02-38216-18119
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Sequence 42169, Application PC/TUS0238216

GENERAL INFORMATION:

APPLICANT: Rosetta Genomics LTD

TITLE OF INVENTION: GENES AND USES THEREOF

TITLE OF INVENTION: GENES AND USES THEREOF

FILE REFERENCE: 55002

CURRENT APPLICATION NUMBER: PCT/US02/38216

CURRENT FILING DATE: 2002-11-12

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: Patentin version 3.2

LENGTH: 22
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GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 41830
LENGTH: 21
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                                                                                                                                                                                                                                                                                             / Match 80.0%; Score 14.4; DB 1; Length 21; Local Similarity 93.8%; Pred. No. 1e+04; nes 15; Conservative 0; Mismatches 1; Indels
  GENES AND USES THEREOF
TITLE OF INVENTION: GENES AND USES THEREOF FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PALENLIN Version 3.2
SEQ ID NO 41829
LENGTH: 21
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Best Local Similarity 93.8%; Pre
Matches 15; Conservative 0;
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CORGANISM: Homo sapiens
PCT-US02-38216-42169
                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-41829
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CORGANISM: Homo sapiens
PCT-US02-38216-41830
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PCT-US02-38216-42169
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Sequence 5724, Application PC/TUS0238216

Sequence 5724, Application PC/TUS0238216

GENERAL INFORMATION:

APPLICANT: ROSetta Genomics LTD

TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY

TITLE OF INVENTION: GENES AND USES THEREOF

FILE REFERENCE: 55002

CURRENT APPLICATION NUMBER: PCT/US02/38216

CURRENT FILING DATE: 2002-11-12

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: Patentin version 3.2

SEQ ID NO 5724
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APPLICANT ROSELLON:

TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY

TITLE OF INVENTION: GENES AND USES THEREOF

FILE REFERENCE: 55002

CURRENT APPLICATION NUMBER: PCT/US02/38216

CURRENT FILING DATE: 2002-11-12

SOFTWARE: Patentin version 3.2

SEQ ID NO 84403

LENGTH: 18

TYPE: DNA

CORGANISM: Homo sapiens

PCT-US02-38216-84403
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Query Match 76.7%; Score 13.8; DB 1; Length 22; Best Local Similarity 88.2%; Pred. No. 1.8e+04; Matches 15; Conservative 0; Mismatches 2; Indels
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Sequence 84403, Application PC/TUS0238216
GENERAL INFORMATION:
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CORGANISM: Homo sapiens
PCT-US02-38216-5724
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Search completed: October 27, 2003, 18:22:55 Job time : 307.029 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1 (bases 1 to 20)
Glazer, P.M.
Methods of targeted mutagenesis using triple-helix forming oligonucleotides
Patent: US 6303376-A 2 16-OCT-2001;
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/note="Sequence can be repeated
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Score 14.2; DB 6;
Pred. No. 2.3e+05;
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Sequence 2 from patent US 6303376.
AR173053 GI:17912544
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Sequence 17 from Patent WO0210452.
AX384817
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Unclassified.
1 (bases 1 to 20)
Glazer,P.M.
Triple-helix forming oligonucleotides for targeted mutagenesis
Patent: US 5962426-A 2 05-OCT-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            Lipford,G.B., Heeg,K. and Wagner,H.
G-motif oligonucleotides and uses thereof
Patent: WO 0014217-A 42 16-MAR-2000;
LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ; WAGNER HERMANN (DE)
CPG IMMUNOPHARMACEUTICALS GMBH (DE)
Location/Qualifiers
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/organism="synthetic construct"

/mol_type="genomic DNA"

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/note="synthetic, no natural origin"

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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="synthetic, no natural oric
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Sequence 2 from patent US 5962426.
AR078333.1 GI:10005079
CPG IMMUNOPHARMACEUTICALS GMBH (DE)
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Sequence 42 from Patent W00014217.
               Location/Qualifiers
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Gaps

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Unclassified.

(bases 1 to 20)

Ballinger, D.G., Ding, W., Wagner, S. and Hess, M.A.
Chromosome 11-linked coronary heart disease susceptibility gene
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Unknown.
Unknown.
Unknown.
I (bases 1 to 20)
Acton, S.Laurene.
Intronic and polymorphic SR-BI nucleic acids and uses therefor
Intronic and polymorphic SR-BI nucleic acids and uses therefor
Patent: US 5998141-A 56 07-DEC-1999;
Location/Qualifiers
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Acton, S. Laurene.
Human intronic and polymorphic SR-BI nucleic acids and uses
therefor
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Pred. No. 4e+05;
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                                                                                     Patent: US 6225451-A 204 01-MAY-2001;
Location/Qualifiers
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Location/Qualifiers
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Sequence 56 from patent US 5998141.
AR092032
AR092032.1 GI:10018786
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Sequence 56 from patent US 6130041.
AR112167
AR112167.1 GI:14092067
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Method and nucleic acids for the analysis of colon cancer
Patent: WO 03014388-A 245 20-FEB-2003;
Epigenomics AG (DE)
Location/Qualifiers
                                                                                                                                             Distler,J., Model,F. and Taubert,H.
Method and nucleic acids for the analysis of colon cancer
Patent: WO 03014388-A 243 20.FEB-2003;
Epigenomics AG (DE)
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/note="Detection oligonucleotide for p16"
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/note="Detection oligonucleotide for pl6"
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Seguence 245 from Patent WO03014388.
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AX705576.1 GI:29562241
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Sequence 243 from Patent WO03014388.
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AX705574,1 GI:29562239
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PAT 16-MAY-2001

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1 (bases 1 to 21)

Matson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.
Oligonucleotide repeat arrays
Oligonucleotide repeat arrays
Patent: US 5981185-A 11 09-NOV-1999;
Location/Qualifiers
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Unknown.
Unclassified.

1 (bases 1 to 21)
Matson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.
Oligonuclectide repeat arrays
Oligonuclectide repeat arrays
Patent: US 5981185-A 12 09-NOV-1999;
Location/Qualifiers
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(bases 1 to 21)

Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
Oligonucleotide repeat arrays
Patent: US 5981185-A 48 09-NOV-1999;
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Sequence 48 from patent US 5981185.
AR084559
AR084559.1 GI:10011330
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Sequence 12 from patent US 5981185.
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ARO84523.1 GI:10011294
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Best Local Similarity 76.2
Matches 16; Conservative
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1 (bases 1 to 20)
Acton, S.L. and Ordovas, J.M.
Human intronic and polymorphic SR-BI nucleic acids and uses therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unclassified.

(bases 1 to 20)

Cohen,D., Chumakov,I. and Blumenfeld,M.
Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
Patent: US 6537751-A 9409 25-MAR-2003;
Location/Qualifiers
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 83.3%; Pred. No. 5.8e+05;
live 0; Mismatches 3;
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Location/Qualifiers
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Sequence 11 from patent US 5981185.
AR084522
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Sequence 56 from patent US 6228581.
AR149209.1 GI:15113800
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13 c l g
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Query Match
Best Local Similarity 76.2%; Pred. No. 6.9e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps

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Search completed: October 27, 2003, 11:09:25 Job time: 439.8 secs

CD28 expression in CD28 inhibiting ph CD28 expression in CD28 inhibiting ph CD28 inhibiting ph CD28 inhibiting ph CD28 inhibiting ph SupF gene triplex-forming oldigonucleotide AG Human androgen rec Apolipoprotein CII Gastric acid produ ASO probe #5 to de Human SR-BI gene e Human ETFB allele-Synthetic oligonuc Protypic blocking Hepatitis C virus Guanine quartet co Guanine quartet se co Guanine quartet co Guanine quartet se co Guanine quartet co Guanine quartet co HSV replication in Peptide nucleic ac CD28 expression in CD28 inhibiting ph Human tissue kalli

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Reduction, T cell, CD28, gene expression, treatment; immune system, disorder, graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, 5'-UTR; systemic lupus erythematosus, inflammatory bowel disease, triplex forming, oligonucleotide, 5'-untranslated region, ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Triplex forming oligo targetting CD28 5'-UTR (nt 58-78).
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         AAX90336
AAT36244
AAX90335
AAX90337
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AAT701074
AAT701074
AAT200125
AAT20025
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AAX24525
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AAX246593
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AAQ50950
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ABK99296
AAQ61991
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95US-0529878.
95US-0387041.
95US-0529878.
96WO-US01507
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(first entry)
 WO9624380-A1.
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18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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15-APR-1997
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Synthetic.
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Triplex forming ol CD28 inhibiting ph CD28 inhibition ol Triplex forming ol CD28 inhibiting ph CD28 inhibition ol Nucleotide sequenc Nucleotide sequenc
                                                               October 27, 2003, 10:32:29 ; Search time 189 Seconds (without alignments) 299.938 Million cell updates/sec
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         GenCore version 5.1.6
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                         The present oligonucleotide reduces T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythemateusus, inflammatory bowel disease, etc. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
(Updated on 25-MAR-2003 to correct PR field.)
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                                                                                           Oligo:nucleotide which reduces CD28 gene expression in T cells - for treating immune system diseases, e.g. graft vs. host disease,
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(ICNC ) ICN PHARM INC
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method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonuclectide used in the exemplification of the
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ive 0; Mismatches 0;
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                                                                      present invention
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The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN) AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; ss.
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                                                                                                 Reduction, T cell, CD28, gene expression, treatment, immune system, disorder, graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, 5'-UTR; systemic lupus erythematosus, inflammatory bowel disease, triplex forming, oligonucleotide, 5'-untranslated region, ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present oligonuclectide reduces T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
(Updated on 25-MAR-2003 to correct PR field.)
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                                                                    Triplex forming oligo targetting CD28 5'-UTR (nt 58-75).
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                                    The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN).

AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                        G-motif oligonucleotide, vaccine, Toxoplasmosis, viral infection, antigen presenting cell activation, natural killer cell; septic shock; cytotoxic T-lymphocyte; inflammation; autoimmune disease; rheumatoid arthritis, Crohn's disease; sarcoidosis; multiple sclerosis; Kawasaki syndrome; graft-versus-host disease; transplant rejection; helper T cell response 1-mediated disease; Lyme arthritis; Streptococcal induced arthritis; chronic inflammatory bowel disease; psoriasis vulgaris; experimental allergic encephalomyelitis; insulin-dependent diabetes mellitus; bacterial infection; parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a G-motif oligonucleotide of the invention. The specification describes compositions comprising G-motif oligonucleotides inhibit activation of antigen presenting cells by inhibiting the uptake of DNA by a cell, by stimulating natural killer cells, or by co-stimulating cytotoxic T-lymphocytes. The G-motif oligonucleotides may be used for the productions of vaccines for treating septic shock, inflammation, autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease, sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Compositions comprising G-motif oligonucleotides useful for treating e.g. septic shock, rheumatoid arthritis, diabetes and human immunodeficiency virus infections -
                                                                                                                                                                                        Gaps
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O
                                                                                                                                                             Score 18; DB 20; Length 18;
Pred. No. 7e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of G-motif oligonucleotide GR1.
                                                                                                                                  Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
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            Claim 5; Column 29; 45pp; English
                                                                                                                                                       Query Match
Best Local Similarity 100.0%; P:
Matches 18; Conservative 0;
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                                                                                                           diseases.
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disease and transplant rejection), helper T cell response 1-mediated diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic inflammatory bowel disease, psoriasis vulgaris, experimental allergic encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis), viral infections (e.g. Cytomegalovirus and human immunodeficiency virus (HIV) -infections), spontaneous abortions and tumours. They may also be used to induce proliferation of bone marrow cells, especially macrophage precursor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G-motif oligonucleotide, vaccine; Toxoplasmosis; viral infection; antigen presenting cell activation; natural killer cell; septic shock; cytotoxic T-lymphocyte; inflammation; autoimmune disease; rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis; Kawasaki syndrome; graft-versus-host disease; transplant rejection; helper T cell response 1-mediated disease; Lyme arthritis; Streptococcal induced arthritis; chronic inflammatory bowel disease; psoriasis vulgaris; experimental allergic encephalomyelitis; insulin-dependent diabetes mellitus; bacterial infection; tumour; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 21; Length 18
Pred. No. 7e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
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Local Similarity 100.0%; P:
les 18; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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in cytokine release. (Updated on 25-MAR-2003 to correct PR field.)
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disease and transplant rejection), helper T cell response 1-mediated diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic inflammatory bowel disease, psoriasis vulgaris, experimental allergic encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis), viral infections (e.g. Cytomegalovirus and human immunodeficiency virus (HIV) -infections), spontaneous abortions and tumours. They may also be used to induce proliferation of bone marrow cells, especially macrophage precursor cells.
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Reduction; T cell; CD28; gene expression; treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; psoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2; systemic lupus erythematosus; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated disease, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction
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                                                                                                                                                         Score 18; DB 21; Length 18;
Pred. No. 7e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                           CD28 expression inhibiting oligonucleotide, RT09s.
                                                                                                                                  Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-2; production; antisense; inhibition; ss
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100.0%; Pre
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95US-0529878.
95US-0387041.
95US-0529878.
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(first entry)
                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 18; Conservative
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18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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16-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                    Gaps
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                                           Length 18;
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94.4%; Pred. No. 2.7e+03;
iive 0; Mismatches 1;
                                          17;
                                        ore 16.4; DB 17
ed. No. 2.7e+03;
Mismatches 1
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Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;
                                           Score
Pred.
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Best Local Similarity 94.4%;
Matches 17; Conservative
                                           78.1%;
94.4%;
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                        Query Match
Best Local Similarity 94.1
Best Local Similarity 17; Conservative
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Reduction; T cell; CD28; gene expression; treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; psoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2; systemic lupus erythematosus; inflammatory bowel disease; IL-2; production; antisense; inhibition; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc. systemic CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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88.9%; Pred. No. 1e+04;
cive 0; Mismatches 2;
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95US-0529878.
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Best Local Similarity 88.9
Matches 16; Conservative
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18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. settmulation of CD28 positive T cells, with a consequent reduction in cytokine release.
(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                             Reduction; T cell; CD28; gene expression; treatment; immune syster disorder; graft versus host disease; septic shock; viral disease; psoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2; systemic lupus erythematosus; inflammatory bowel disease; ID-2; production; antisense; inhibition; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligo:nucleotide which reduces CD28 gene expression in T cells - for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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8B.9%; Pred. No. 1e+04;
iive 0; Mismatches 2;
                                                                                                CD28 expression inhibiting oligonucleotide, RT05s.
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18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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16-APR-1997
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16-APR-1997
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          AAT36242;
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US5932556-A

expression inhibiting oligonucleotide, RT10s.

CD28

XEXPEXEX

AAT36244

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Length 18; Indels ô

Gaps

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of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonucleotide used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ81074 is the supF gene triplex forming mutagenic oligonucleotide pso-AGT20. It forms a triplex (a triple stranded nucleic acid) with a specific site on the supF genome, enabling the covalently bound 4'hydroxymethyl-4,5',8-trimethylpsoralen group to produce a site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              supF gene; triplex forming mutagenic oligonucleotide; pso-AGT20;
4'hydroxymethyl-4,5',8-trimethylpsoralenated; site specific; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             supF gene triplex forming mutagenic oligonucleotide pso-AGT20.
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Pred. No. 1.7e+04;
D; Mismatches 3;
                                                                                                                                                                          70.5%; Score 14.8; DB 20; ilarity 88.9%; Pred. No. 1e+04; Conservative 0; Mismatches 2;
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"4'hydroxymethyl-4,5',
8-trimethylpsoralenated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specific mutation. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                           Sequence 18 BP; 1 A; 2 C; 11 G; 4 T; 0 other;
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84.2%;
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Best Local Similarity 84.2
Matches 16; Conservative
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es 16; Conserv
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AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothioate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention describes a method for inhibiting the expression
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                                                                                                                                                                                                                                                                                                                                                                                                                             present invention.
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ri Li	AZ645874 1M0511C07	AZ766712 1M0564A03	AZ871408 2M0184E16	AZ666896 1M0549A24
		Description	AZ645874 1M0511C	AZ766712	AZ871408	AZ666896
SUMMARIES		ID	14.6 69.5 22 28 AZ645874	AZ766712	AZ871408	AZ666896
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
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1M0564A03R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0564A03 R, genomic survey sequence.
AZ766712
AZ766712.1 GI:12884063
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
Unpublished
                                                                                                                                                                                                                                                                                                                                       /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: C column: 07
Seg primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0511C07"
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Best Local Similarity
Matches 17; Conserv
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(a) (bases 1 to 22)
(bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGC1M library"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Best Local Similarity 81.0%; Pred. No. 3.1e+05;
Matches 17; Conservative 0; Mismatches 4;
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0564 row: A column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
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/strain="C57BL/6J"
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/clone="UUGC1M0564A03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse_10kb_plasmid_UUGCIM_library"/note="Vector: PWD42nv; Purified genomic_DNA_from M.musculus_C57BL/6J_(male) was obtained_from the Jackson
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0184 row: E column: 16
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Pers
                                                                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                                                                                                            'mol_type="genomic DNA"
'strain="CS7BL/6J"
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clone="UUGC2M0184E16"
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                                                                                                                                                                                                                                                                                                                                                                          sex="Male"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab host="E. Coll strain XLIO-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGC1M library"/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Class: plasmid ends
High quality sequence stop: 20.
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/db_xref="taxon:10090"
/clone="UUGCIM0549A24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0
Matches 16; Conservative
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'sex="Male
                   University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/61 (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ476392 1M0295F12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0295F12 F, genomic survey sequence.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                        S. 2030 E., SLC,
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                    Biomedical Polymers Research Bldg., 20
Rm. 308, Biomeurc.
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0242 row: O column: 12
Seq primer: CGTTGTAAAACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
. 20.
"Mis musculus"
                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/61"
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Contact: Robert B. Weiss
University of Utah Genome Center
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/clone="UUGC2M0242012"
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us-09-331-204a-6.szlm22.rst

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Query Match
Best Local Similarity
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AZ331988
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1 (bases 1 to 22)

1 (bases 1 to 22)

2 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., and Radelof,U.

2 Orbungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

3 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes plant J. 32 (5), 845-857 (2002)

3 Contact: Weisshaar B

ADIS DNA core facility at MPIZ

Max-Plantchine Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaa@mpiz-koeln.mpg.de
    Insert Length: 22 Std Error: 0.00
    Plate: 2 row: K column: 08
    Seq primer: SP6; CATACGATTTAGGTGACACTATAG.

Location/Qualifiers
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line
Ph.D. student, Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                              /issue_type="infiltrating ductal carcinoma"
/lab host="DH10B"
/clone lib="NCI CGAP Br5"
/note="Organ: breast; Vector: pAMP10; mRNA made from infiltrating ductal carcinoma, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. "
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Pred. No. 6.2e+05;
0; Mismatches 4; Indels
                                                                                                                                                                                            Trace considered overall poor quality Insert Length: 255 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1377515"
/sex="female"
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80.0%;
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Best Local Similarity 80.00,
Thes 16; Conservative
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Beta vulgaris
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BQ585098
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/lab_mosure_mbnubaros
/clone_lib="MPIZ-ADIS-024-inflorescence"
/clone_lib="MPIZ-ADIS-024-inflorescence"
/note="Vector: pcMvSpORT6; Site_1: Sal1; Site_2: Not1;
cDNA_library_from_sugar_beet, library_provided_by_KWS
Kleinwanzlebener_Saatzucht_AG_Einbeck, Germany, contact:
b.schulz@kws.de; cloning_sites_Sal1-Not1, primer_sites_and
orientation:
Sp6-Sal1-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Not1-T7; Note:
Sequencing_granted_in_the_context_of_the_GABI-Beet_project_, local_PI: Dr. Katharina_Schneider, coordinator: Prof.
christian_Jung; Sequence_submission_managed_by
RZPD/GABI-Primary_database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Musinae; Mus.

1 (bases 1 to 22)

1 (bases 1 to 22)

1 (bases 1 to 22)

2 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

3 Silam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

4 M., Rose,M., Rose,R.,

5 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

6 Unpublished

7 Contact: Robert B. Weiss

7 Unpublished

8 University of Utah Genome Center

8 University of Utah

8 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

8 H112, USA
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0
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Pred. No. 6.2e+05;
0; Mismatches 5;
                         db_xref="taxon:161934"
/clone="024-002-K08"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0060 row: B column: 11
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/clone="UUGC1M0060B11"
/sex="Male"
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Location/Qualifiers
xref="GABI:181599"
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          Laborators C. Junale) was colcained from the Dackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1); a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0429D18R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0429D18 R, genomic survey sequence.
AZ607348

AZ607348.1 GI:11729538
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished
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musculus C57B1/6J (male) was obtained from the Jackson
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0429 row: D column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Mus.
1 (bases 1 to 22)
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Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                           musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/note="Vector: PWD42nv; Purified genomic DNA from M.
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80.0%; Pred. No. 6.2e+05;
tive 0; Mismatches 4; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0180 row: E column: 12
Seg primer: CACACAGGAAACAGCTATGACC
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Best Local Similarity 80.0
Matches 16; Conservative
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Fax: 801 585 7177
Email: ddunn@genet
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Beta vulgaris
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                                                          Inductible Carlot DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

Mouse whole genome scaffolding with paired end reads from 10kb
                    /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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clone_lib="Mouse 10kb plasmid UUGC1M library"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0282 row: O column: 04
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
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Matches 16; Conservative
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database: http://gabi.rzpd.de
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76.2%;
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Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, J.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
fingerprinting allows access to 25 000 potential sugar beet genes
Contact: Weisshaar B
ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062881
Email: weisshaa@mpiz-koeln.mpg.de
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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-Not1, primer sites and
orientation:
SP6-Sall-CCAGGGTCG-Sprime-cDNA-polyA-CC-Not1-T7; Note:
Sequencing granted in the context of the GABI-Beet project
, local PI: Dr. Katharina Schneider, coordinator: Prof.
Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
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/clone lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DV391392
E012713-024-017-014-T7 MPIZ-ADIS-024-storage root Beta vulgaris CDNA clone 024-017-014 3-PRIME, mRNA sequence.
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SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet project
local PI: Dr. Katharina Schneider, coordinator: Prof.
Christian Jung; Sequence submission managed by
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/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line
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Beta vulgaris
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BQ591392/c
LOCUS
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VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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Deta vulgaris

Sw Beta vulgaris

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

Caryophyllales; Amaranthaceae; Beta.

I {bases 1 to 21}

Sherwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,

Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.

and Radelof, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

Contact: Weisshaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaa@mpiz-koeln.mpg.de

Insert Length: 21 Std Error: 0.00

Plate: 17 row: P column: 09

Seq primer: 77; GTAATACGACTATAGGGC.

Location/Onalifiers
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SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Notl-T7; Note:
Sequencing granted in the context of the GABI-Beet project
, local PI: Dr. Katharina Schneider, coordinator: Prof.
Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Kleinwanzlebener_Saatzucht_AG_Einbeck, Germany, contact:
b.schulz@kws.de; cloning_sites_SalI-Not1, primer_sites_and
                                                                                                                                                                                                                                                                                                                                                                         BQ591421
E012714-024-017-P09-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-017-P09 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Beta vulgaris"
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Score 13; DB 13; Length Ar Pred, No. 9.5e+05;
                                                                                           0; Mismatches
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Search completed: October 27, 2003, 13:59:26 Job time: 1847.4 secs Sequence Sequence

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Run on:

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Sequence 19, Appli
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Sequence 17, Appl
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Sequence 36, Appl
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Sequence 24, Appl
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Sequence 3, Appli
Sequence 1, Appli
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Patent No. 5932556

GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:
ADDRESSEE: Crockett & Fish
STREET: 3000 S. Augusta Court
CITY: La Habra
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 21; DB 2; Best Local Similarity 100.0%; Pred. No. 4.1; Matches 21; Conservative 0; Mismatches 0;
US-08-886-161-16

US-09-194-478-7

US-09-194-478-8

US-09-194-478-8

US-09-194-478-8

US-08-632-575B-19

US-08-632-575B-19

US-08-855-825-17

US-09-629-644A-175

US-08-863-639A-73

US-08-103-663-24

US-08-013-801-4

US-08-013-801-4
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION NUMBER: 33,880
REFERENCE/DOCKET NUMBER: 213/003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-525-3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
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US-08-529-878B-4
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Sequence 3, Appl
Sequence 2, Appli
Sequence 204, App
Sequence 56, Appl
Sequence 56, Appl
Sequence 56, Appl
Sequence 56, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 48, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 46, Appl
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Sequence 45, Appl
                                                                                                           October 27, 2003, 10:32:34; Search time 48.2 Seconds (without alignments) 192.304 Million cell updates/sec
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Compugen Ltd.
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US-08-529-878B-45
US-08-529-878B-44
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US-09-476-712-2
US-09-476-713-204
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US-08-403-888A-117
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US-09-013-55A-57
US-09-0130-57
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                                                                                                                                                                                                                                                                                              569978 seqs, 220691566 residues
                 GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
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Match Length
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Sequence 44, Application US/08529878B

Sequence 44, Application US/08529878B

Patent No. 5932556

JETCHE OF INVENTION:
APPLICANT: Tam, Robert C.
TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Crockett & Fish
STREET: 3000 S. Augusta Court
CITY: La Habra
STREET: 3000 S. Augusta Court
COUNTRY: United States of America
ZIP: 90631
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: NordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fish, Robert D.
REFERENCE/DOCKET NUMBER: 213/003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFHONE: 714-525-3433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.7%; Score 18; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 85.7%; Score 18; DB 2; Best Local Similarity 100.0%; Pred. No. 58; Matches 18; Conservative 0; Mismatches
13-SEP-1995
                    APPLICATION NUMBER: US/08/529, FILING DATE: 13-SEP-1995 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION: NAME: Fish, Robert D. REFERENCE/DOCKET NUMBER: 213/0 TELEPHONE: 714-525-3433 TELEFAX: 714-525-3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 TTGGAGGGGTGGTGGGG 21
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                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
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TELEFAX: 714-525-3303
     CURRENT APPLICATION DATA:
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TOPOLOGY: unk
MOLECULE TYPE:
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100.0%; Score 21; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 21; Conservative 0; Mismatches 0; Indels
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US-08-529-878B-45

Sequence 45, Application US/08529878B

Patent No. 5932556

GENERAL INFORMATION:

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES:

ADDRESSE: ADDRESS:
ADDRESSE: Crockett & Fish STREET: 3000 S. Augusta Court CITY: La Habra STREET: D. Habra STREET: California COUNTRY: United States of America STATE: California COUNTRY: United States of America STATE: Plopy disk COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk COMPUTER: IBM PC COMPath:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fish, Robert D.
REFERENCE/DOCKET NUMBER: 213/003
TELEPHONE: 714-525-3303
TELEPHONE: 714-525-3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 90631
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfert
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SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
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Sequence 204, Application US/09262773
Sequence 204, Application US/09262773
Sequence 204, Application US/09262773
Sequence 204, Application US/09262773
Sequence 204, Application:
APPLICANT: Ballinger, Dennis G.
APPLICANT: Wagner, Susanne
APPLICANT: Wagner, Susanne
APPLICANT: Hess, Mark A.
TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
FILE REFERENCE: Myriad 3
CURRENT APPLICATION NUMBER: US/09/262,773
CURRENT FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 210
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              COMPUTEY: USA

ZIP: 30309-3450

ZIP: 30309-3450

ZIP: 30309-3450

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

CURRENT APPLICATION NUMBER: US/09/411,291

FILING DATE: CURNOWN>

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: YUll4

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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Pred. No. 2.8e+03;
0; Mismatches 4;
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Pred. No. 1.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (404)-873-9
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
COGANISM: DNA fragment
US-09-262-773-204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-411-291-2
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Sequence 2, Application US/08476712

Sequence 2, Application US/08476712

Patent No. 5962426

GENERAL INFORMATION:

TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for CORRESPONDENCE 6

CORRESPONDENCE 6

CORRESPENCES FATERET 2800 One Atlantic Center STREET: 2800 One Atlantic Center STATE: GA

COUNTRY: USA

COUNTRY: USA

CONPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: BM PC compatible COMPUTER: BM PC compatible COMPUTER: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: 1US/08/476,712

FILING DATE: 7-JUNE-1995

CLASSIPETATION: 514

PATCHORNEY APPLICATION NUMBER: 1US/08/476,712
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                          Indels
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Pred. No. 1.7e+03;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
     Pred. No. 58;
                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: YUll'
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARKSTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
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Best Local Similarity 100.0%;
Matches 18; Conservative 0
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Best Local Similarity 84.2%;
Matches 16; Conservative (
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EDNESS: single
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TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-476-712-2
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APPLICANT: Acton, Susan L.
APPLICANT: Acton, Susan L.
APPLICANT: Acton, Jose M.
TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
FILE REFERENCE: MIA-005.04
CURRENT APPLICATION NUMBER: US/09/031,626
CURRENT PILING DATE: 1998-02-27
EARLIER APPLICATION NUMBER: 08/890,979
EARLIER FILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin Ver. 2.0
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; Patent NO. 6130041
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
; TITLE OF INVENTION SR-BI NUCLEIC ACIDS AND USES THEREFOR
; CURRENT APPLICATION NUMBER: US/09/032,894
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,980
; BARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
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83.3%; Pred. No. 4e+03;
cive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 13.2; DB 3;
Pred. No. 4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                              35,430
ER: MIA-005.02
FILING DATE: 10-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REGISTRATION INFORMATION:
TELEPHONE: 617-832-1000
T
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Patent No. 6228581
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GTTGGAGGGGTGGTGGG 20
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Best Local Similarity 83.3%;
Matches 15; Conservative
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Best Local Similarity 83.3
Matches 15; Conservative
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; ORGANISM: Human
US-09-032-894-56
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US-09-032-894-56/c
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LENGTH: 20
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                                                                        Sequence be, Application US/UBBSUDENCE
Sequence be, Application US/UBBSUDENCE
SEQUENCES
SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELLOT LLP
STREET: One Post Office Square
CITY: BOSTON
STREET: One Post Office Square
CITY: BOSTON
STREET: One Post Office Square
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: MA
COUNTRY: USA
ZIP: PROPOUTER: FLOPPY disk
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DEP COMPATIBLE
COUNTRY: USA
ZIP: MA
COUNTRY: USA
ZIP: MA
COUNTRY: USA
ZIP: MA
COUNTRY: USA
ZIP: MA
COUNTRY: USA
ZIP: OLOPY-109
COUNTRY: USA
ZIP: OLOPE-1997
COUNTRY: USA
ZIP: MA
COUNTRY: SATATION: A35
COUNTRY: APPLICATION NUMBER: USA-005.01
TELEPHONE: 617-832-1000
TELEPHONE: 617-832-1000
TELEPHONE: 617-832-1000
TELEPHONE: 617-832-1000
TELEPHONE: 617-832-1000
TELEPHONE: G17-832-1000
TELEPHONE: G17
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Patent No. 6030778
GENERAL INFORMATION:
APPLICANT: Acton, Susan L.
APPLICANT: Ordovas, Jose M.
TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS TITLE OF INVENTION: DISORDERS
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DB 2; Length 20;
4e+03;
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ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 62.9%; Score 13.2; Best Local Similarity 83.3%; Pred. No. 4e Matches 15; Conservative 0; Mismatche
                                                       Sequence 56, Application US/08890980
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US-08-890-979-56/c
                   US-08-890-980-56/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-890-980-56
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APPLICANT: Reddy, Parameswara M.
APPLICANT: Hanna, Naeem B.
TITLE OF INVENTION: Methods and Reagents
TITLE OF INVENTION: for Cleaving and
TITLE OF INVENTION: Deprotecting
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.9%; Score 13; DB 76.2%; Pred. No. 4.86 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beckman Instruments, Inc
2500 Harbor Boulevard
                                                                                                                                  US/07/873,915A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/257,964
                                                                                                                                                                                                                                                                     128D-111
                    MEDIUM TYPE: L.C. COMPUTER: IBM OPERATING SYSTEM: MS.DOS SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/873,9 FILING DATE: 19920424 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION: NAME: BURGOON, Richard P. REFERENCE/DOCKET NUMBER: 128D-TELEPHONE: (714) 773-7610 TELEPHONE: (714) 773-7936 INFORMATION: TELEPHONE: (714) 773-7936 INFORMATION: TELEFAX: (714) 773-7936 INFORMATION: TELEFAX: (714) 773-7936 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 21 bases TYPE: NUCLEIC ACID STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 92634
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 Mb
   Diskette, 3.5 inch, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGTTGGAGGGGGTGGTGGGG 21
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; Sequence 3, Application US/08257964
; Patent No. 5518651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 773-6971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM
OPERATING SYSTEM: MS.DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/2
FILING DATE: June 8, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34,347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Fullerton
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 16; Conserv
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   MEDIUM TYPE:
MEDIUM TYPE:
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US-07-873-915A-3
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LOCATION: 1..20

CHER INFORMATION: downstream amplification primer 99-449 for SEQ 1544, in complemen

US-09-422-978-9409
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-04-21
EARLIER FILING DATE: 1998-04-21
NUMBER: OF SEQ ID NOS: 11796
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                                                                                                                                                                                Gaps
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                                                                                                                                  62.9%; Score 13.2; DB 3; Length 20;
83.3%; Pred. No. 4e+03;
                                                                                                                                                                               Indels
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Patent No. 5348868
GENERAL INFORMATION:
APPLICANT: Reddy, Parameswara M.
TITLE OF INVENTION: Methods and Reagents
TITLE OF INVENTION: for Cleaving and
TITLE OF INVENTION: Deprotecting
TITLE OF INVENTION: Oligonucleotides
                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                          5-09-422-978-9409/c
Sequence 9409, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
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                                                                                                                                  Query Match 62.9
Best Local Similarity 83.3
Matches 15; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Beckman I
STREET: 2500 Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 92634
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Fullerton
STATE: California
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-031-626-56
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US-07-873-915A-3
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US-08-863-639A-11/C
US-08-863-639A-11/C
US-08-863-639A-11/C
SEQUENCE 11, Application US/08863639A
Patent No. 5981185
Fatent No. 5981185
FAPLICANT Cassin, Peter J.
APPLICANT Rampel, Jang B.
STREET: 22 SQUINCEDOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES:
STREET: 225 SOUTH Lake Avenue, 9th Floor
CINTRY: Pasadena
STREET: 225 SOUTH Lake Avenue, 9th Floor
CONPUTER: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: DISKETER: DISK
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                                                                                                                                                                                                                                                                                                                                                                             Query Match 61.9%; Score 13; DB 1; Length 21; Best Local Similarity 76.2%; Pred. No. 4.8e+03; Matches 16; Conservative 0; Mismatches 5; Indels
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STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid

US-08-863-639A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGGTTGGAGGGGGTGGTGGGG 21
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                                                                  TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: no

ANTI-SENSE: no

US-08-257-964-3
SEQUENCE CHARACTERISTICS:
LENGTH: 21 bases
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Search completed: October 27, 2003, 14:03:34 Job time : 48.2 secs

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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/DSO7_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO96_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USO96_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/USO96_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/USO96_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/USO96_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/USO96_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/USO96_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/USO08_NEW_PUB.seq:*

17: /cgn2_6/ptodata/1/pubpna/USO08_NEW_PUB.seq:*

16: /cgn2_6/ptodata/1/pubpna/USO08_NEW_PUB.seq:*

17: /cgn2_6/ptodata/1/pubpna/USO08_NEW_PUB.seq:*

16: /cgn2_6/ptodata/1/pubpna/USO08_NEW_PUB.seq:*

17: /cgn2_6/ptodata/1/pubpna/USO08_NEW_PUB.seq:*
                             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1792395 segs, 1340900451 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                               OM nucleic - nucleic search, using sw model
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21
1 999ttggaaggggtggtggtgg 21
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 22
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Sequence:
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		Description	Sequence 22, Appl	Sequence 56, Appl	56,	2132	Sequence 2133, Ap	Sequence 2422, Ap	Sequence 2423, Ap	Sequence 2132, Ap	Sequence 2133, Ap	Seguence 2422, Ap	Sequence 2423, Ap	à	Sequence 26, Appl	30	Sequence 26, Appl	59,
SUMMARIES		ID	US-09-874-162A-22	US-09-779-152-56	US-10-023-610-56	US-09-740-332-2132	US-09-740-332-2133	US-09-740-332-2422	US-09-740-332-2423	US-09-817-879-2132	US-09-817-879-2133	US-09-817-879-2422	US-09-817-879-2423	US-09-828-034-31	US-10-059-877-26	US-10-303-109A-30	US-10-059-888-26	US-10-204-884-59
		DB	101	11	14	11	11	11	13	12	12	12	12	σ	12	12	14	12
		Length DB	20	20	20	17	17	17	17	17	17	17	17	21	17	17	17	18
	% Ouerv	Match	63.8	62.8	62.9	61.9	61.9	61.9	61.9	61.9	61.9	61.9	61.9	61.9	61.0	61.0	61.0	61.0
		Score	13.4	13.2	13,2	13	13	13	13	13	13	13	13	13	12.8	12.8	12.8	12.8
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RESULT 2
US-09-779-152-56/c
; Sequence 56, Application US/09779152
; Publication No. US20030044782A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.

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19 GGAGGGGGTGATGGG

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Sequence 35, Sequence 13, Sequence 20, Sequence 22, Sequence 22, Sequence 22, Sequence 22, Sequence 22, Sequence 23, Sequence 23, Sequence 295, Sequence 295, Sequence 24, Sequence 133, Sequence 24, Sequence 133,	
17 12.8 61.0 20 14 US-10-181-846-35 18 12.8 61.0 22 11 US-09-988-115A-120 2 12.8 61.0 22 11 US-09-988-115A-120 2 2 12.6 60.0 22 11 US-09-988-115A-120 2 2 12.6 60.0 21 US-09-988-115A-20 2 2 12.6 60.0 21 US-09-988-115A-20 2 2 12.6 60.0 21 US-09-988-115A-20 3 2 2 2 60.0 21 US-09-988-115A-20 4 2 2 60.0 21 US-09-988-115A-20 5 2 2 60.0 21 US-09-988-115A-20 5 2 2 6 60.0 21 US-09-988-115A-20 5 2 2 6 60.0 21 US-09-988-115A-20 5 2 2 6 60.0 21 US-09-988-115A-20 5 3 12.2 58.1 17 10 US-09-988-25-966 5 3 12.2 58.1 17 10 US-09-988-26-95-96 5 3 12.2 58.1 17 10 US-09-988-26-95-96 5 3 12.2 58.1 17 10 US-09-988-26-95-96 6 12.2 58.1 17 10 US-09-988-26-95-96 7 12.2 58.1 17 10 US-09-988-26-95-96 8 12.2 58.1 17 10 US-09-988-26-95-96 9 12.2 58.1 12 10 US-09-966-37-99 9 12.2 58.1 12 10 US-09-966-37-99 10 12.2 58.1 12 10 US-09-966-37-99 11 12 57.1 20 10 US-09-966-37-99 12 57.1 20 10 US-09-966-37-99 13 57.1 20 10 US-09-966-37-99 14 12 57.1 20 10 US-09-966-37-99 15 17 17 US-09-99-916-666-2 16 17 17 US-09-916-666-2 17 17 10 US-09-916-666-2 18 12 57.1 20 US-09-916-666-2 18 17 17 10 US-09-916-666-2 18 17 17 10 US-09-916-666-2 18 17 17 17 17 17 17 18 18 18 18 18 18 18	Qy 6 GGAGGGGTGGTGG 20

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Sequence 2422, Application US/09740332

Sequence 2422, Application US/09740332

Publication No. US20030125270A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals Inc.

TITLE OF INVENTION: Hepatitis C Virus Infection

FILE REFERENCE: RPI 400/003

CURRENT APPLICATION NUMBER: US/09/740,332

CURRENT FILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 9704

SOFTWARE: Patentin version 3.0

SEQ ID NO 2422

LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-740-332-2133/c
; Sequence 2133, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Hepatitis C Virus Infection
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2133
; LENGTH: 17
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Pred. No. 3.3e+04;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature

LOCATION:

OTHER INFORMATION: oligonucleotide substrate

US-09-740-332-2133
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                                                                                                                                     OTHER INFORMATION: oligonucleotide substrate US-09-740-332-2132
                                                                                                                                                                                                    Query Match 61.9%; SC
Best Local Similarity 100.0%; P
Matches 13; Conservative 0;
LENGTH: 17
TYPE: RNA
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: RNA
ORGANISM: artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: RNA
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                  9 GGGGGTGGTGGGG 21
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                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION:
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US-09-740-332-2422
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US-09-740-332-2132/c
; Sequence 2132, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Hepatitis C virus Infection
; TITLE OF INVENTION: Hepatitis C virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2132
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                 APPLICANT: MCCATLLY, Jeanette J.
TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
FILE REFERENCE: MNI-172CP2
CURRENT APPLICATION NUMBER: US/09/779,152
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: 08/890,979
PRIOR APPLICATION NUMBER: 08/890,979
PRIOR FILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 56
LENGTH: 20
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Publication No. US20030023059A1

GENERAL INFORMATION:

APPLICANT: Acton, Susan L.

TITLE OF INVENTION:

FILE REFERENCE: MA-005.03

CURRENT APPLICATION NUMBER: US/10/023,610

CURRENT FILING DATE: 2001-12-17

EARLIER APPLICATION NUMBER: 09/686,106

EARLIER PILING DATE: 2000-10-10

EARLIER PILING DATE: 1998-02-27

EARLIER PILING DATE: 1998-02-27

EARLIER PILING DATE: 1997-07-10

NUMBER OF SEQ ID NOS: 121

SOFTWARE: Patentin Ver. 2.0

LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                        Score 13.2; DB 11;
Pred. No. 2.7e+04;
0; Mismatches 3;
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Best Local Similarity 83.3%;
Matches 15; Conservative
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ORGANISM: Human
US-10-023-610-56
                                                                                                                                                                                                                                                                                                  ; TYPE: DNA; ORGANISM: Human US-09-779-152-56
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US-10-023-610-56/c
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Sequence 2133, Application US/09817879; Sequence 2133, Application US/09817879; Publication No. US20030171311A1
; Beneral Information:
    APPLICANT: Ribozyme Pharmaceuticals Inc.
    TITLE OF INVENTION: Hepatitis C Virus Infection
    TITLE OF INVENTION: Hepatitis C Virus Infection
    FILE REFERENCE: MBHB00-801-F
    CURRENT APPLICATION NUMBER: US/09/817,879
    CURRENT APPLICATION NOS: 9703
    SOFTWARE: Patentin version 3.0
    SEQ ID NO 2133
    LENGTH: 17
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Publication No. US20030171311A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBHB00-801-F
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84.6%; Pred. No. 3.3e+04;
live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2422, Application US/09817879; Sequence 2422, Application US/09817879; Publication No. US20030171311A1; GENERAL INFORMATION:
TITLE OF INVENTION: Hepatitis C Virus Infection; TILE REFERENCE: MBH800-801-F; CURRENT APPLICATION NUMBER: US/09/817,879; CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703; SOFTWARE: PatentIn version 3.0; SEQ ID NO 2422; LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2133
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ORGANISM: artificial sequence
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ORGANISM: artificial sequence
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Best Local Similarity 100.
Matches 13; Conservative
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Matches 11; Conserv
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US-09-817-879-2423
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US-09-817-879-2422
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Sequence 2132, Application US/09817879
Publication No. US20030171311A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Hepatitis C virus Infection
FILE REFERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
SEQ ID NO 2132
                                                                                                                                                                                                                         Sequence 2423, Application US/09740332
Sequence 2423, Application US/09740332
Publication No. US20030125270A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Hepatic Nucleic Acid Treatment of Diseases or Conditions Relate TITLE OF INVENTION: Hepaticis C Virus Infection
FILE REPERENCE: RPI 400/003
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: PatentIn version 3.0
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Query Match 61.9%; Score 13; DB 11; Length 17; Best Local Similarity 84.6%; Pred. No. 3.3e+04; Matches 11; Conservative 2; Mismatches 0; Indels
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Pred. No. 3.3e+04;
2; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
ORGANISM: artificial sequence
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Best Local Similarity 84.6%;
Matches 11; Conservative
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LENGTH: 17
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CTHER INFORMATION: Description of Artificial Sequence:/No. US20030157490Ale = CTHER INFORMATION: synthetic construct US-10-059-877-26
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US-10-303-109A-30/c
; Sequence 30, Application US/10303109A
; Publication No. US20030194726A1
; GENERAL INFORMATION:
; APPLICANT: BOLCHAKOVA, Elena
; APPLICANT: ROZZELLE, James
; TITLE OF INVENTION: Thermus Oshimai Nucleic Acid Polymerases
; FILE REFERENCE: 4777US
; CURRENT APPLICATION NUMBER: US/10/303,109A
; CURRENT FILING DATE: 2002-11-22
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 30
; LENGTH: 17
                                                                                                                                                                                                                                                                                                                                  Length 17;
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87.5%; Pred. No. 4e+04;
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         PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 08/856,141
PRIOR FILING DATE: 1997-05-14
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 17
                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Matches 14; Conservative
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ORGANISM: Thermus oshimai
US-10-303-109A-30
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-31
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                                                                                                                                                                                                                                                                                                                        Score 13; DB 12; Length 17
Pred. No. 3.3e+04;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31, 37, 99 Sequence 31, 38 PELICANT: Zhong, Weidong APPLICANT: Hong, Zhi CURRENT APPLICATION HOWBER: US/09/828,034 CURRENT FILING DATE: 2001-04-06 PRIOR APPLICATION NUMBER: U.S. 60/195,852 PRIOR FILING DATE: 2000-04-06 NUMBER OF SEQ ID NOS: 33 SOFTWARE: Patentin Ver. 2.1 LENGTH: 21
                                                                                                                                                                                                          ) NAME/KEY: misc_feature

; LOCATION:

; OTHER INFORMATION: oligonucleotide substrate

US-09-817-879-2423
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
SEQ ID NO 2423
LENGTH: 17
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Best Local Similarity 84.6%;
Matches 11; Conservative
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US-09-828-034-31/c
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Sequence 26, Application US/10059888
; Publication No. US20030025882A1
; GENERAL INFORMATION:
; APPLICANT: CHAO, LEE
; APPLICANT: CHAO, JULIE
; APPLICANT: CHAO, JULIE
; APPLICANT: CONS. JULIE
; APPLICANT: CONS. JULIE
; APPLICANT: SONG, OING
; TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL
; TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL
; TITLE OF INVENTION: US/10/059,888
; TITLE OF INVENTION: US/10/059,888
; CURRENT APPLICATION NUMBER: US/10/059,888
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 09/495,140
; PRIOR FILING DATE: 2000-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 09/389,566
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 08/856,141
PRIOR FILING DATE: 1997-05-14
                                                                                                    Sequence 26, Application US/10059877
Sequence 26, Application US/10059877
Sublication No. US20030157490A1
GENERAL INFORMATION:
APPLICANT: CHAO, LEE
APPLICANT: CHAO, JULIE
APPLICANT: CHAO, JULIE
APPLICANT: CHAO, JULIE
APPLICANT: SONG, QING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING
TITLE OF INVENTION: HYPERTENSION
TITLE OF INVENTION: HYPERTENSION
FILE REFERENCE: 19113.0081U2
CURRENT APPLICATION NUMBER: US/10/059,877
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: 09/495,140
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 09/389,566
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RESULT 13 US-10-059-877-26

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// NUMBER OF SEQ ID NOS: 31
// SOFTWARE: FastSEQ for Windows Version 4.0
// SEQ ID NO 26
// LENGTH: 17
// TYPE: DNA
// ORGANISM: Artificial Sequence
// Organis
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| cgn2_6/ptodata1/lpna/PCTUS_COMB.seq:*
| cgn2_6/ptodata1/lpna/VSOT_COMB.seq:*
| cgn2_6/ptodata1/lpna/VSOT_COMB.seq:*
| cgn2_6/ptodata1/lpna/VSOT_COMB.seq:*
| cgn2_6/ptodata1/lpna/VSOB_COMB.seq:*
| cgn2_6/ptodata1/lpna/VSOB_C
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 nucleic search, using sw model
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Perfect score:
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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cgn2_6/ptodata/1/pna/US101B_COMB.seq:
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cgn2_6/ptodata/1/pna/US101B_COMB.seq:
cgn2_6/ptodata/1/pna/US101B_COMB.seq:
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cgn2_6/ptodata/1/pna/US101B_COMB.seq:
cgn2_6/ptodata/1/pna/US101B_COMB.seq:
cgn2_6/ptodata/1/pna/US101B_COMB.seq:
cgn2_6/ptodata/1/pna/US6001_COMB.seq:
cgn2_6/ptodata/1/pna/US6012_COMB.seq:
cgn2_6/ptodata/1/pna/US6013_COMB.seq:
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Match
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Sequence 4, Appli Sequence 6, Appl Sequence 6, Appl

US-08-387-041A-4 9 US-09-331-204-6 9 US-09-331-204A-6 US-08-387-041A-3

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Sequence 186, App
Sequence 2660, App
Sequence 186, App
Sequence 2660, App
Sequence 2360, App
Sequence 2340, App
Sequence 27360, App
Sequence 18278, App
Sequence 47426, App
Sequence 40745, App
Sequence 40745, App
Sequence 1853, App
Sequence 1853, App
Sequence 1865, App Sequence 18418, App Sequence 18552, App Sequence 185552, App Seque
                                                                                                                                                     Sequence 5, Applisequence 5, Applisequence 8, Applisequence 9, Applisequence 9, Applisequence 10, Applisequence 17, Applisequence 17, Applisequence 117, Applisequence 117, Applisequence 1189, A Sequence 11817, A Sequence 5, Applisequence 5, Applisequen
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GENERAL INFORMATION:
APPLICANT: Tam, Robert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION
TITLE OF INVENTION: OF CD28 EXPRESSION
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/387,041A

FILING DATE: 02-FEB-1995

CLASSIFICATION: 514
US-09-331-204-1
US-09-331-204A-4
US-09-786-436-17
US-09-786-436-42
US-09-786-426-42
US-09-331-204A-8
US-08-172-676-17
US-08-10-310-188-51871
US-08-463-519-5
US-10-310-188-5389
US-10-310-188-5389
US-10-310-188-5389
US-08-463-519-5
US-08-463-519-5
US-08-668-235-2660
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
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NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
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APPLICANT: ICN Pharmaceuticals, Inc.

APPLICANT: ICN Pharmaceuticals, Inc.
APPLICANT: Tam, Robert
TITLE OF INVENTION:
FILE REFERENCE: 216/013-US1
CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT FILING DATE: 1999-08-20
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09331204
GENERAL INFORMATION:
APPLICANT: Tam, Robert
TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
TITLE OF INVENTION: IMMUNE RESPONSE
FILLE REFERENCE: ICNSequence
CURRENT APPLICATION NUMBER: US/09/331,204
CURRENT PILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 21
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Pred. No. 1.1e+03
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              TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-360
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
HOLECULE TYPE: DNA (genomic)
US-08-387-041A-4
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1 Similarity 100.0%;
21, Conservative 0,
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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21; Conserv
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S-09-331-204-1
S-guence 1, Application US/09331204
GENERAL INFORMATION:
APPLICANT: Tam, Robert
TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN TITLE OF INVENTION: IMMUNE RESPONSE
FILE REFERENCE: ICNSequence
CURRENT APPLICATION NUMBER: US/09/331,204
CURRENT FILING DATE: 1999-08-20
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                                      Length 21;
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                                     Score 21; DB 19;
Pred. No. 1.1e+03;
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Best Local Similarity 100.0%; Pred. No. Matches 18; Conservative 0; Mismatc)
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                                    Query Match
Best Local Similarity 100.0%;
Matches 21; Conservative 0
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-6
                                                                                                                        RESULT 4
US-08-387-041A-3
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General Application US/09331204A

General Information

General Information

General Information

General Information

General Information

Applicant: Tam, Robert

TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Resp

FILE REFERENCE: 216/013-US1

FILE REFERENCE: 216/013-US1

CURRENT APPLICATION NUMBER: US/08/331,204A

CURRENT FILING DATE: 1999-08-20

PRIOR APPLICATION NUMBER: PCT/US97/23927

PRIOR FILING DATE: 28

SOFTWARE: Patentin version 3.0

SEQ ID NO 4

LENGTH: 18
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APPLICANT: Wagner, Hermann
APPLICANT: Lipford, Grayson
APPLICANT: Heeg, Klaus
TITLE OF INVENTION: G-Motif Oligonucleotides and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: C1041/7010 (AMS)
CURRENT APPLICATION NUMBER: US/09/786,436
CURRENT FILING DATE: 2001-03-02
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
FEMALE OF 10 NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 0;
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Pred. No. 1.2e+04
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      PCT/US97/23927
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Best Local Similarity 100.0%; P:
Matches 18; Conservative 0;
PRIOR APPLICATION NUMBER: PCT/US
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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CORGANISM: synthetic construct
US-09-331-204A-4
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Sequence 7, Application US/09331204A; Sequence 7, Application US/09331204A; Genence 7, Application US/09331204A; General Information:
APPLICANT: ICN Pharmaceuticals, Inc., APPLICANT: Tam, Robert
TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Rest; FILE REFERENCE: 216/013-US1
CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT FILING DATE: 1999-020
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: ICN Pharmaceuticals, Inc.
APPLICANT: Tam, Robert
TITLE OF INVENTION:
G-rich Oligo Aptamers and Methods of Modulating an Immune Resp.
FILE REFERENCE: 216/013-US1
CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR APPLICATION NUMBER: PCT/US97/23927
NUMBER OF SEQ ID NOS: 28
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Pred. No. 1.7e+05;
0; Mismatches 2;
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Pred. No. 4.
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APPLICANT: ICN Pharmaceuticals, Inc.; APPLICANT: Tam, Robert; TITLE OF INVENTION: G-rich Oligo Ap; FILE REFERENCE: 216/013-US1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA; ORGANISM: synthetic construct US-09-331-204A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 78.1%;
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: synthetic construct
US-09-331-204A-8
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   17; Conservative
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SEQ ID NO 8
LENGTH: 18
   Matches
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TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN

TITLE OF INVENTION: IMMUNE RESPONSE

FILE REFERENCE: ICNSequence

CURRENT APPLICATION NUMBER: US/09/331,204

CURRENT APPLICATION NUMBER: PCT/US97/23927

FRIOR APPLICATION NUMBER: PCT/US97/23927

FRIOR APPLICATION NUMBER: PCT/US97/23927

FRIOR FILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.0

LENGTH: 18

TYPE: DNA

TYPE: DNA

TYPE: DNA
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OTHER INFORMATION: Description of Artificial Sequence: An oligomer;
OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic;
OTHER INFORMATION: acid. This term includes oligomers consisting of;
OTHER INFORMATION: naturally occurring bases, sugars and intersugar (US-09-331-204-5
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                                                                                                 DB 33; Length 18;
1.2e+04;
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APPLICANT: Lipford, Grayson
APPLICANT: Lipford, Grayson
APPLICANT: Heeg, Klaus
TITLE OF INVENTION: G-Motif Oligonucleotides and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: C1041/7010 (AWS)
CURRENT APPLICATION NUMBER: US/09/786,436
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: PCT/EP99/06502
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 85.7%; Score 18; DB 33; I
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 0;
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-786-436-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: Synthetic oligonucleotide US-09-786-436-42
                                                                                             Query Match 85.7%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 1.2 Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                           Sequence 42, Application US/09786436 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-09-331-204-5
; Sequence 5, Application US/09331204
; GENERAL INFORMATION:
                                                                                                                                                                                             TTGGAGGGGGTGGTGGGG 21
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ORGANISM: Artificial Sequence
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Best Local Similarity
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LENGTH: 18
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US-09-331-204-4
; Sequence 4, Application US/09331204
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
; TITLE OF INVENTION: IMMUNE RESPONSE
; FILE REFERENCE: ICNSequence
; CURRENT APPLICATION NUMBER: US/09/331,204
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: An oligomer OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic OTHER INFORMATION: acid. This term includes oligomers consisting of OTHER INFORMATION: naturally occurring bases, sugars and intersugar (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3043, Application US/10303778
GENERAL INFORMATION:
APPLICANT: RosettaGenomics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
FILE REFERENCE: 47416
CURRENT APPLICATION NUMBER: US/10/303,778
CURRENT FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 17608
SOFTWARE: Patentin version 3.1
SEQ ID NO 3043
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CURRENT APPLICATION NUMBER: US/09/331,204A CURRENT FILING DATE: 1999-08-20 PRIOR APPLICATION NUMBER: PCT/US97/23927 PRIOR FILING DATE: 1997-12-19 NUMBER OF SEQ ID NOS: 28 SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                ENGTH: 18
TYPE: DNA
CORGANISM: SYNTHETIC CONSTRUCT
US-09-331-204A-9
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CRGANISM: Homo sapiens
US-10-303-778-3043
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US-10-303-778-3043
                                                                                                           NUMBER SOFTWARE: Pa
SEQ ID NO 9
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ENGTH: 19
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Sequence 78687, A
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Sequence 51871, P
Sequence 27376, P
Sequence 41647, P
Sequence 46976, P
Sequence 26689, P
Sequence 26689, P
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Sequence 55389,
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                                                                                       October 27, 2003, 11:09:34 ; Search time 358.2 Seconds (without alignments) 97.777 Million cell updates/sec
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/cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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PCT-US02-38216-51871
PCT-US02-38216-57376
PCT-US02-38216-41647
PCT-US02-38216-41647
PCT-US02-38216-48943
PCT-US02-38216-48943
PCT-US02-38216-78687
US-09-978-3338-2
US-09-978-3338-2
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seg length: 22
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38216-39492 Sequence 39493 Sequence 5724 Sequence 5724 Sequence 5724 Sequence 5724 Sequence 5724 Sequence 5724 Sequence 5725 Sequence 5736 Sequence 5184 Sequence 5189 Sequence 5189 Sequence 6107 Sequence 6107 Sequence 6107 Sequence 6885 Sequence 6107 Sequence 6885 Sequence 6985 Sequence 6985 Sequence 6985 Sequence 5726 Sequence 6985 Sequence 6985 Sequence 6985 Sequence 6985 Sequence 572 Sequence 6985 Sequ	PCT-US02-38216-39492 Sequence 5724 PCT-US02-38216-57248 Sequence 5724 PCT-US02-38216-57248 Sequence 5724 PCT-US02-38216-53577 Sequence 38923 PCT-US02-38216-53577 Sequence 5357 PCT-US02-38216-5362 Sequence 5357 PCT-US02-38216-57364 Sequence 5736 PCT-US02-38216-5736 Sequence 5736 PCT-US02-38216-5736 Sequence 5736 PCT-US02-38216-51842 Sequence 5184 PCT-US02-38216-51842 Sequence 5184 PCT-US02-38216-61077 Sequence 6107 PCT-US02-38216-68378 Sequence 6107 PCT-US02-38216-686378 Sequence 6885 PCT-US02-38216-68952 Sequence 6985 PCT-US02-38216-69453 Sequence 6985 PCT-US02-38216-26725 Sequence 2672	4.8 22 1 PCT-US02-38216-59492 Sequence 59492 3.8 18 1 PCT-US02-38216-10539 Sequence 57243 3.8 18 1 PCT-US02-38216-57248 Sequence 57243.8 18 1 PCT-US02-38216-53392 Sequence 57243.8 20 1 PCT-US02-38216-5357 Sequence 53573.8 21 1 PCT-US02-38216-57364 Sequence 53573.8 21 1 PCT-US02-38216-57364 Sequence 57363.8 22 1 PCT-US02-38216-10603 Sequence 57363.8 22 1 PCT-US02-38216-57364 Sequence 57363.8 22 1 PCT-US02-38216-57364 Sequence 57363.8 18 1 PCT-US02-38216-57364 Sequence 51842 2.9 18 1 PCT-US02-38216-51842 Sequence 518942 Se	6 64.8 22 1 PCT-US02-38216-39492 Sequence 59492 6 64.8 22 1 PCT-US02-38216-57248 Sequence 5724 6 63.8 18 1 PCT-US02-38216-57248 Sequence 5724 6 63.8 19 1 PCT-US02-38216-5827 Sequence 5357 6 63.8 20 1 PCT-US02-38216-51804 Sequence 5357 6 63.8 21 1 PCT-US02-38216-55622 Sequence 5180 7 6 63.8 21 1 PCT-US02-38216-57364 Sequence 5736 7 6 63.8 21 1 PCT-US02-38216-57364 Sequence 5736 7 6 62.9 18 1 PCT-US02-38216-5736 Sequence 5736 7 6 62.9 18 1 PCT-US02-38216-51842 Sequence 5180 7 6 62.9 18 1 PCT-US02-38216-5180 Sequence 5180 7 6 62.9 18 1 PCT-US02-38216-5180 Sequence 5180 7 6 62.9 18 1 PCT-US02-38216-61077 Sequence 6107 7 6 62.9 18 1 PCT-US02-38216-61077 Sequence 6107 7 62.9 19 1 PCT-US02-38216-69453 Sequence 6105 7 62.9 1 PCT-US02-38216-69453 Sequence 6105 7 62.9 1 PCT-US02-38216-69453 Sequence 6105 7 62.9 1 PCT-US02-38216-69453 Sequence 6105 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	~	•	•	•	•	٠.	-	٠.	~		-	Α,	~	-	-	~	~	~	~
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		22	3.6 64.8 22 1 PCT- 3.6 64.8 22 1 PCT- 3.4 63.8 18 19 1 PCT- 3.4 63.8 20 1 PCT- 3.2 62.9 18 1 PCT- 3.3 62.9 18 1 PCT- 3.4 63.8 PCT- 4.4 63.8 PCT- 4.5 FCT- 5.5 FCT- 5.6 F	-38216-3949	-38216-5724	-38216-1053	-38216-3892	-38216-5357	-38216-418	38216-5562	-38216-5736	-38216-1060	-38216-973	-38216-2953	-38216-5184	-38216-5189	-38216-6107	-38216-8637	-38216-6885	02-38216-6945	02-38216-1056	02-38216-2672

ALIGNMENTS

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APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 51871
LENGTH: 22
                        Sequence 41819, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: ROSetta Genomics LTD
TITLE OF INVENTION:
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT PILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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GENERAL INFORMATION:
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ORGANISM: Homo sapiens
PCT-US02-38216-41819
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PCT-US02-38216-51871
RESULT 1
PCT-US02-38216-41819
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PCT-US02-38216-51871
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APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 46976
LENGTH: 19
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; Sequence 26689, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 26689
; LENGTH: 22
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Pred. No. 1.8e+04;
                                                                                       Score 14.4; DB 1;
Pred. No. 1.8e+04;
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Best Local Similarity 93.8%;
Matches 15; Conservative
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Best Local Similarity 93.8%;
Matches 15; Conservative
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CORGANISM: Homo sapiens
PCT-US02-38216-26689
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                         ; ORGANISM: Homo sapiens
PCT-US02-38216-38943
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Matches 15; Conserv
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; TYPE: DNA
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GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 38943
LENGTH: 19
                                                                                                                                        Sequence 27376, Application PC/TUS0238216
Sequence 27376, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 27376
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT APPLICATION NUMBER: PCT/US02/38216
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 41647
LENGTH: 18
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Pred. No. 1.8e+04;
0; Mismatches 1;
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 GGGTTGGAGGGGGTGGTGGGG
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Best Local Similarity 93.8%;
Matches 15, Conservative
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ORGANISM: Homo sapiens
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PCT-US02-38216-27376
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PCT-US02-38216-41647
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Sequence 2, Application US/09978333C

GENERAL INFORMATION:
GENERAL INFORMATION:
TILE OF INVENT: Glazer, Peter M.
TILE OF INVENTION: Triple-Helix Forming Oligonucleotides for Targeted Mutagenesis
FILE REFERENCE: YU 132
CURRENT APPLICATION NUMBER: US/09/978,333C
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 09/411,291
PRIOR APPLICATION NUMBER: US 08/476,712
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
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84.2%; Pred. No. 2.1e+04;
iive 0; Mismatches 3;
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Pred. No. 2.1e+04;
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Sequen
            0; Mismatches
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US-09-978-333C-2
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ORGANISM: Artificial Sequence
FEATURE:
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Matches 16; Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
                  16; Conservative
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PCT-US02-38216-51847
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Sequence 2, Application US/09978333B
Sequence 2, Application US/09978333B
Sequence 2, Application US/09978333B
APPLICANT: Glazer, Peter M.

TITLE OF INVENTION: Triple-Helix forming Oligonucleotides for Targeted Mutagenesis
FILE REFERENCE: YU 132
CURRENT APPLICATION NUMBER: US/09/978,333B
CURRENT FILING DATE: 1099-10-04
PRIOR FILING DATE: 1999-10-04
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 20
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| Sequence 78687, Application PC/TUSO238216
| Sequence 78687, Application PC/TUSO238216
| GENERAL INFORMATION:
| APPLICANT: Rosetta Genomics LTD
| TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
| FILE PEFERENCE: 55002
| CURRENT APPLICATION NUMBER: PCT/USO2/38216
| CURRENT FILING DATE: 2002-11-12
| NUMBER OF SEQ ID NOS: 86841
| SOFTWARE: Patentin version 3.2
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Pred. No. 2.1e+04;
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Pred. No. 2.1e+04;
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TITLE OF INVENTION: GENES AND USES THEREOFFILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 42141
LENGTH: 22
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ORGANISM: Artificial Sequence
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Matches 16; Conservative
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PCT-US02-38216-78687
                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
PCT-US02-38216-42141
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LENGTH: 19
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Search completed: October 27, 2003, 18:22:55 Job time: 358.2 secs
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 63940
LENGTH: 22
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GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
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Pred. No. 2.1e+04;
0; Mismatches 3; Indels
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Best Local Similarity 84.2%; Pred. No. 2.1e+04;
Matches 16; Conservative 0; Mismatches 3;
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 55389
LENGTH: 21
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Best Local Similarity 84.2%;
Matches 16; Conservative
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PCT-US02-38216-63940
                                                                                                                                                               TYPE: DNA
CORGANISM: Homo sapiens
PCT-US02-38216-55389
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PCT-US02-38216-27360
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PCT-US02-38216-63940
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PCT-US02-38216-27360
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LENGTH: 19
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GenCore version 5.1.6
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41: em_nugo_ouner:.. Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

tion	1974 Sy 131393	BD001798 Immunogen	AX532425 Sequence AX532426 Sequence	AX532427 Sequence	AX023427 Sequence	AR029938 Sequence AX532424 Sequence	AX532428 Sequence	AR232303 Sequence AX214604 Sequence	AX214605 Sequence	AX21545/ Sequence AX215458 Sequence	AX215459 Sequence	AX532429 Sequence	AX214603 Sequence AX215452 Sequence	AR126724 Sequence	AX03345/ Sequence AX037370 Sequence	AX037374 Sequence	AXZ41159 Sequence AX486754 Sequence	AR072479 Sequence	AR084552 Sequence	AR084570 Sequence	AR084575 Sequence	AR084581 Sequence AR084594 Sequence	Sequence	igonucle	A12052 Oligonucieo AX729881 Sequence	Sequence	IO7756 Sequence 12 AX154328 Sequence	Sequenc	ARII6659 Sequence	Sequenc		C C C C C C C C C C C C C C C C C C C	linear FAT US-COL-LYVE			genomes of types HIV-I, HIV-2 ication of these genomes and infections
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SUMMARIES	A31974 AR131393	BD001798	AX532426	AX532427	AX023427	AR029938 AX532424	AX532428	AR232303 AX214604	AX214605	AX215457 AX215458	AX215459	AX532429	AX214603 ax215452	AR126724	AX033457 AX037370	AX037374	AX241159 AX486754	AR072479	AR084552 Ab004664	AR084570	AR084575	AR084581 AR084594	AR097224	A12051	A12052 AX729881	AX739210	107756 ax154328	AX298242	AR116659	AR237949	ALIGNMENTS		zı op agnosis primer.			agnier, L. ss of retroviral sfor the amplific of these viral i
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PAT 22-NOV-2002
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  PD 04-APR-2000
PF 24-SEP-1999 JP 1999270165
PR 02-JUN-1989 FR 89/07354,20-SEP-1989 FR 89/12371 PI
MAURICE MONCANY, LUC MONTAGNIER
PC C12N15/09, A61K39/21, A61K48/00, A61P31/18, C07H21/04, C07K14/155, PC C07K14/16,
PC C12Q1/68, C12Q1/70, G01N33/569, C12N15/00
CC
FH Key Location/Qualifiers
FT source 1. 21
/organism='Artificial Sequence'.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Patent: EP 1239051-A 1934 11-SEP-2002;
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AX532426
AX532426.1 GI:25256627
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EP1239051.
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/mol type="genomic DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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Sequence 1934 from Patent
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Homo sapiens
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I (bases 1 to 21)

NRS Moncany, M. and Montagnier, L.

Moncany, M. and Montagnier, L.

Mucleotide sequences derived from the genome of retroviruses of the amplification of the genomes of their uses in particular for the amplification of the genomes of these retroviruses and for the in vitro diagnosis of the diseases due to these viruses

NNAL Patent: US 6194142-A 45 27-FEB-2001;

Location/Qualifiers
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Immunogenic compounds containing a translation product of
nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and SIV
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BD001798.1 GI:18626357
JP 2000093187-A/45.
synthetic construct
artificial sequences.
1 (bases 1 to 21)
Moncany, M. and Montagnier, L.
Immunogenic compounds containing a translation product of nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and incleotide sequence from retrovirus genome of HIV-1, HIV-2 and incleotide sequence from retrovirus genome of HIV-1, HIV-2 and incleotide sequence from retrovirus genome of HIV-1, HIV-2 and incleotide sequence from retrovirus genome of HIV-1, HIV-2 and incleotide sequence from retrovirus genome of HIV-1, HIV-2 and incleotide sequence from retrovirus genome of HIV-1, HIV-2 and incleotide sequence from retrovirus genome of HIV-1, HIV-2 and incleotide sequence from retrovirus genome of HIV-1, HIV-2 and incleotide sequence from retrovirus genome of HIV-1, HIV-2 and incleotide sequence from retrovirus genome of HIV-1, HIV-2 and incleotide sequence from retrovirus genome of HIV-1, HIV-2 and incleotide sequence from retrovirus genome of HIV-1, HIV-2 and incleotide sequence from retrovirus genome of HIV-1, HIV-2 and incleotide sequence from retrovirus genome of HIV-1, HIV-2 and incleotide sequence from retrovirus genome of HIV-1, HIV-2 and incleotide from retrovirus genome of HIV-1, HIV-1, HIV-2 and incleotide from the HIV-1, HIV-1, HIV-1, HIV-1, HIV-1, HIV-1, HIV-1, HIV-1
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Patent: JP 2000093187-A 45 04-APR-2000;
INST PASTEUR,INST NATL DE LA SANTE & DE LA RECHERCHE MEDICAL
OS Artificial Sequence
PN JP 2000093187-A/45
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Patent: EP 0403333-A 29 19-DEC-1990;
INSTITUT PASTEUR; INSTITUT NATIONAL DE LA SANTE
MEDICALE (INSERM)
Location/Qualifiers
                                                                                                                                                                                                                                                                               Score 15.4; DB 6;
Pred. No. 2.7e+04;
0; Mismatches 1;
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/organism="synthetic construct"
/mol_type="genomic DNA"
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Sequence 45 from patent US 6194142.
AR131393 GI:14120296
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Best Local Similarity 94.1%;
Matches 16; Conservative
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artificial sequences.
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
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Unclassified.
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Best Local Similarity
Matches 16; Conserv
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AX023427/c
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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G-motif oligonucleotides and uses thereof
Patent: WO 0014217-A 17 16-MAR-2000,
LIPFORD GRAYSON B (DE); HEEG KLAUS (DE); WAGNER HERMANN (DE)
CPG IMMUNOPHARMACEUTICALS GMBH (DE)
LOCATION/Qualifiers
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Pred. No. 4.2e+04;
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Shannon,M.
Human posh-like protein 1
Patent: EP 1239051-A 1935 11-SEP-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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Patent: EP 1239051-A 1936 11-SEP-2002;
Acomica, Inc. (US)
Location/Qualifiers
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AX532427
AX532427.1 GI:25256629
                                                                     /organism="Homo sapiens"
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/db_xref="taxon:9606"
a 12 c 0 g 4
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Sequence 17 from Patent WO0014217.
AX023402
AX023402.1 GI:10183802
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/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Parthology Parthy 100.0%; Parthy 100.0%; Parthyle 0;
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Best Local Similarity 100.
Matches 15; Conservative
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AX532427/C
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AX023402
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G-motif oligonucleotides and uses thereof
Patent: WO 0014217-A 42 16-MAR-2000,
LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ; WAGNER HERMANN (DE)
CPG IMMUNOPHARMACEUTICALS GMBH (DE)
Location/Qualifiers
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Wang,C.-G. and Hepburn,A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US 5861244-A 127 19-JAN-1999;
Location/Qualifiers
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/note="synthetic, no natural origin"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="synthetic, no natural origin"
/ no c 13 g 4 t
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Pred. No. 5e+04;
0; Mismatches
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88.9%; Pred. No. 5e+04;
live 0; Mismatches
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Seguence 127 from patent US 5861244.
AR029938
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Sequence 42 from Patent WO0014217
AX023427
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PAT 07-SEP-2001
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 46 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
1. 17
/organism="synthetic construct"
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//note="Nucleic Acid"
//note="Nucleic Acid"
                                                                                                      Unclassified.
Unclassified.
1 (bases 1 to 20)
McKay,R., Freier,S.M. and Wyatt,J.
Antisense modulation of casein kinase 2-alpha prime expression
Patent: US 6455307-A 93 24-SEP-2002;
Location/Qualifiers
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20 bp
Sequence 93 from patent US 6455307.
AR232303
AR232303.1 GI:27274295
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Sequence 47 from Patent WO0159103.
AX214605
AX214605.1 GI:15524648
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Sequence 46 from Patent WO0159103.
AX214604
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/organism="unknown"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human posh-like protein 1

Human posh-like protein 1

Patent: EP 1239051-A 1937 11-SEP-2002;

Acomica, Inc. (US)

Location/Qualifiers

1. 17

/organism="Homo sapiens"
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/db_xref="taxon:9606"

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Fatent: EP 1239051-A 1933 11-SEP-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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EP1239051.
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Sequence 1937 from Patent EP1239051.
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i a 11 c 1 g 4
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AX532424
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AX532428.1 GI:25256631
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                           GGAAGGGGAGGAGGGG 1
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FEATURES

REFERENCE

RESULT 12 AR232303

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Blatt,L., Mcswiggen,J. and Chowrira,B.M.
Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression

L Patent: WO 0159103-A 47 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)

Location/Qualifiers

1. .17

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/note="Mucleic Acid"

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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 899 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
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Search completed: October 27, 2003, 11:09:26 Job time : 377.114 secs

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October 27, 2003, 10:32:29; Search time 1581.77 Seconds (without alignments) 276.576 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                  OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AI251781 qu76g01.x AZ876923 2M0192D07 AI582080 ar96b07.x AZ468862 1M0282004
SUMMARIES	c 1 13.8 76.7 19 9 AI251781 2 13.8 76.7 22 28 AZ876923 c 3 13.4 74.4 22 9 AI582080 4 13.2 73.3 21 28 AZ468862
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Z345792 1M008	AZ760597 1M0554N21	Z786308 2M003	12326 1M035	Z645269 1M051	Z659755 1M053	Z772707 1M058	Z969440 2M024	Z476392 1M029	Z583408 1M037	Z653464 1M052	Z774703 2M000	Z871715 2M018	Z969578 2M024	Z307952 1M001	Z331988 1M006	Z607348 1M042	Z645874 1M051	Z871408 2M018	996014 os26d0	Z797469 2M005)1245 hasp (Z666896 1M054	911600 od90d0	568336 cn68h0	2766712 1M056	758301 ty06a0	Z783420 2M002	254493 AU2544	Z387199 1M014	Z394677 1M015	ZS12534 1M035	434548 ti49d0	473941 tm04c1	735392 at10e1	2585098 E0118	Z447246 1M0244E2	Z512762 1M0358	Z845320 2M0145M0	968729 or69h11.	2955804 2M0222L	
8 AZ34579	0	8 AZ78630	8 AZ51232	8 AZ64526	8 AZ65975	8 AZ772707	8 AZ96944	8 AZ47639	8 AZ58340	8 AZ65346	8 AZ77470	8 AZ87171	8 AZ96957	8 AZ30795	8 AZ33198	8 AZ60734	8 AZ64587	8 AZ87140	AA996014	8 AZ79746	3 BQ9012	8 AZ66689	AA91160	A156833	8 AZ7667	AI758301	8 AZ7834	AU25449	8 AZ38719	8 AZ3946	8 AZ51253	AI43454	AI47394	AI73539	3 BQ58509:	8 AZ44724	8 AZ5127	8 AZ84532	AA96872	A7955	
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ALIGNMENTS

RESULT 1	
AI251781/c	
rocus	AI251781 19 bp mRNA linear EST 05-NOV-1998
DEFINITION	qu76g01.x1 NCI CGAP Brn35 Homo sapiens cDNA clone IMAGE:1978032 3'
	similar to TR: 039949 039949 HYDROXYPROLINE-RICH PROTEIN. ;, mRNA
	sequence.
ACCESSION	AI251781
VERSION	AI251781.1 GI:3848310
KEYWORDS	BST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
	Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
REFERENCE	1 (bases 1 to 19)
AUTHORS	NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute / National Institute of Neurological
	Disorders and Stroke, Brain Tumor Genome Anatomy Project
	(CGAP/BTGAP), Tumor Gene Index
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D.
	Email: cgapbs-r@mail.nih.gov
	unknown library type
	Trace considered overall poor quality
	Seq primer: -40UP from Gibco
	High quality sequence stop: 1.
FEATURES	Location/Qualifiers
source	ठार. र

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1 TIGGAGGGGGAGGIGGG 17
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Sall;
/site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.33 kb. Tumor types include:
meningioma, oligodendroglioma, astrocytoma (grade II),
medulloblastoma, astrocytoma (grade IV). Life Technologies
catalog #: 11544-012"
4 a 14 c 0 g 1 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ876923
2M0192D07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0192D07 F, genomic survey sequence.
AZ876923
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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88.2%; Pred. No. 5.5e+05;
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Insert Length: 10000 Std Error: 0.00
Plate: 0192 row: D column: 07
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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organism="Mus musculus"
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University of Utah Genome Center
University of Utah
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ar96b07.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173429 3' similar to SW:FOR4_MOUSE Q05859 FORMIN 4 ;contains element MSR1 repetitive element ;, mRNA sequence.
AI582080
AI582080.1 GI:4567977
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1 (bases 1 to 22)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
This clone is available poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
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/db_xref="taxon:9606"
/clone="IMAGE:2173429"
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                                                                                                                                                                            Query Match 73.3
Best Local Similarity 83.3
Matches 15; Conservative
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Fax: 801 585 7177
Email: ddunn@genet
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                                                                                                          BASE COUNT
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AUTHORS
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KEYWORDS
SOURCE
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AZ345792
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Eukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Mus.

1 (bases 1 to 21)
S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                               AZ468862 21 bp DNA linear GSS 04-OCT-2000 1M0282004F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0282004 F, genomic survey sequence.
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[5, AATTCACTAGTAAT 3' and 5' ATTACTAGTG 3'], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library constructed by Bob Barstead."
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                      . 0
                                                                                                                                                          Length 22;
                                                                                             2 others
                                                                                                                                                                                                    Indels
                                                                                                                                                        74.4%; Score 13.4; DB 9; ilarity 87.5%; Pred. No. 7.2e+05; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0282 row: O column: 04
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0282004"
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USA
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Matches 14; Conserv
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                                                                                                                                                             Query Match
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KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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COMMENT
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AUTHORS
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AZ468862
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was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi[4732114]gb|AF129072.1), a copy-number
with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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19 bp DNA linear GSS 29-SEP-2000
1M0080G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0080G12 R, genomic survey sequence.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rosse, M., Rosse, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
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/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
                                                                                                                                                                                                                                                          Score 13.2; DB 28;
Pred. No. 8.3e+05;
0; Mismatches 3;
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Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: G column: 12
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
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/mol type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080G12"
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us-09-331-204a-8.szlm22.rst

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AZ760597
AZ760597.1 GI:12868613
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inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
Plate: 0554 row: N column: 21
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGCIMO554N21"
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genet
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LOCUS
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AUTHORS
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COMMENT
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was hydrodynamically sheares/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0031B17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0031B17 R, genomic survey sequence.
AZ786308
AZ786308.1 GI:12923936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,R., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                              Length 19;
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                                                                                                                                                                                                                                                                          ch 11.1%; Score 12.8; DB 28; I Similarity 87.5%; Pred. No. 1.1e+06; 14; Conservative 0; Mismatches 2;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0031 row: B column: 17
Seg primer: CACACAGGAAACAGCTATGACC
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/organism="Mus musculus"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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High quality sequence stop: 19.
Location/Qualifiers
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us-09-331-204a-8.szlm22.rst

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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1M0357118R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0357118 R, genomic survey sequence.
A2512326
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musculus C57BL/6J (male) was obtained from the Jackson
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0357 row: I column: 18
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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Matches 14; Conservative C
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TITLE

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COMMENT

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1. 20

/organism="Mus musculus"

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/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi |4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases I to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Plate: 0510 row: B column: 10
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
/http://www.jax.org/resources/documents/dnares/). The DNA
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Lunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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1M0537F22F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0537F22 F, genomic survey sequence.
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Insert Length: 10000 Std Error: 0.00
Plate: 0537 row: F column: 22
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Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Mus musculus
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Best Local Simil
Matches 14;
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ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Insert Length: 10000 Std Error: 0.00
Plate: 0583 row: L column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
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20 bp DNA linear GSS 27-APR-2001
2M0242012F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0242012 F, genomic survey sequence.
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musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20.84112, USA
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0242 row: O column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
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Mus musculus
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
/http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
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1M0295F12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0295F12 F, genomic survey sequence.
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Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
... 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., 6
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0295 row: F column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
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High quality sequence stop: 2
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longares,R., Stokes,R., Tingey,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb. plasmid inserts
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0378 row: N column: 23
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Class: plasmid ends
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84112, USA
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pubm42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Weiss Sole, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
RM. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
121: 801 S85 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ653464 21 bp DNA linear GSS 14-DEC-2000 1M0527G11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic 2010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
,M., Rose, M., Rose, R.,
and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.1%; Score 12.8; DB 28; Length 21; 87.5%; Pred. No. 1.1e+06; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0527 row: G column: 11
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0527G11"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 71.1%; Score 12.8; DB 28; Length 21; Best Local Similarity 87.5%; Pred. No. 1.1e+06; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps

BASE COUNT ORIGIN 0

Search completed: October 27, 2003, 13:59:28 Job time : 1582.77 secs us-09-331-204a-8.szlm22.rni

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unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-529-878B-3
                                                                                                                                                                                                                                                                                                                 JS-08-529-878B-3
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8661266666666444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Appli
Sequence 44, Appli
Sequence 4, Appli
                                                                                        // Search time 41.3143 Seconds
(without alignments)
192.304 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 174
Sequence 174
Sequence 45,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3
Sequence 3
Sequence 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-529-878B-3
US-08-529-878B-4
US-08-529-878B-4
US-09-629-878B-4
US-09-629-878B-4
US-09-629-878B-45
US-09-629-64-174
US-09-022-077-45
US-08-184-138-37
US-08-484-138-37
US-08-484-138-37
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US-08-632-575B-19
US-08-632-575B-19
US-08-632-575B-19
US-08-68-913-2
US-08-486-913-2
US-08-486-913-2
US-08-486-913-2
US-08-486-536-2
                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                    569978 seqs, 220691566 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                 - nucleic search, using sw model
                                                                                          October 27, 2003, 10:32:34
                                                                                                                                                                                              IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                       ttggaggggaggtgggg 18
                                                                                                                                                                                                                                                                                                                                                                                    Patents_NA:*
                                                                                                                                            US-09-331-204A-8
18
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                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 22
                                                                                                                                                                                                                                                                                                                                                                                   Issued
                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB 9
Maximum DB 9
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                                                                                                                                                                         Sequence:
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                                                                                            Run on:
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No.
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              Sequence 3, Appli
Sequence 117, Appli
Sequence 117, Appli
Sequence 117, Appli
Sequence 117, Appli
                                                                                                                                                                         Sequence 348, App
Sequence 22, Appl
Sequence 22, Appl
Sequence 66, Appl
Sequence 101, App
Sequence 101, App
Sequence 2, Appli
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Sequence 348, 7
Sequence 22, App
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08529878B

Sequence 3, Application US/08529878B

GENERAL INFORMATION:

APPLICANT: Tam, Robert C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: Crockett & Fish

STREET: 3000 S. Augusta Court

CITY: La Habra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16.4; DB 2;
Pred. No. 1.6e+02;
0; Mismatches 1;
US-08-486-913-3
US-08-300-484-3
US-08-300-484-3
US-08-486-885-3
US-08-486-885-3
US-08-486-33
US-09-780-173A-93
PCT-US95-11234-3
US-08-363-240A-117
US-08-363-240A-117
US-08-363-240A-117
US-08-557-210A-1
US-08-557-210A-1
US-08-95-140-22
US-09-495-1418-101
US-08-927-561-101
US-08-927-561-101
                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United states of America
ZIP: 90631
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fish, Robert D.
REGISTRATION NUMBER: 213/003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-525-3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 base pairs
      CITY: La Habra
STATE: California
COUNTRY: United Sta
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Sequence 45, Application US/08529878B

Patent No. 593256

GENERAL INFORMATION:

APPLICANT: Tam, Robert C.

ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES: 4 ADDRESSEE: Crockett & Fish STREET: 3000 S. Augusta Court CITY: La Habra STATE: California COUNTRY: United States of America STATE: California COUNTRY: United States of America COUNTRY: United States of America STATE: P0631

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE FORM:

MEDIUM TYPE: APPLICATION DATA:

CURSIFICATION NUMBER: 223/083

FILING DATE: 13-SEP-1995

CLASSIFICATION NUMBER: 213/003

FEFERENCE/DOCKET NUMBER: 213/003

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 91.1%; Score 16.4; DB 2; Best Local Similarity 94.4%; Pred. No. 1.6e+02; Matches 17; Conservative 0; Mismatches 1;
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                    APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fish, Robert D.
REGISTRATION NUMBER: 33,880
REFERENCE/DOCKET NUMBER: 213/003
TELEPHONE: 714-525-3433
TELEFAX: 714-525-3303
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TTGGAGGGGGAGGTGGGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic
                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
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                                                                                            Patent No. 5932556

GENERAL INFORMATION:
APPLICANT: Tam, Robert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Crockett & Fish
STREET: 3000 S. Augusta Court
CITY: La Habra
STATE: California
COUNTRY: United States of America
2727: 20631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Deptication US/08529878B
Patent No. 5932556
GENERAL INFORMATION:
APPLICANT: Tam, Robert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Crockett & Fish
STREET: 3000 S. Augusta Court
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fish, Robert D.
REGISTRATION NUMBER: 213/003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-525-3433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: La Habra
STATE: California
COUNTRY: United States of America
ZIP: 90631
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
                    RESULT 2
US-08-529-878B-44
; Sequence 44, Application US/08529878B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TTGGAGGGGGGGGGG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-529-878B-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
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US-09-092-077-45
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 US-09-092-077-45
                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                       Gaps
                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Lex M. Cowsert
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION:
ANTISENSE MODULATION OF PTPIB EXPRESSION
FILE REFERENCE: RTS-0093
CURRENT APPLICATION NUMBER: US/09/487,368A
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 240
LENGTH: 20
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APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Brett P. Monia
APPLICANT: Radeline M. Butler
APPLICANT: Robert McKay
TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
FILE REFERENCE: ISPH-0478
CURRENT APPLICATION NUMBER: US/09/629,644A
CURRENT FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 242
SEQ ID NO 174
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 13.8; DB 4; Length 20; Pred. No. 1.7e+03; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 76.7%; Score 13.8; DB 3; Length 20; Best Local Similarity 88.2%; Pred. No. 1.7e+03; Matches 15; Conservative 0; Mismatches 2; Indels
                     1; Indels
Best Local Similarity 94.4%; Pred. No. 1.6e+02; Matches 17; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
CTHER INFORMATION: Antisense Oligonucleotide
US-09-487-368A-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Antisense Oligonucleotide US-09-629-644A-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-629-644A-174

Sequence 174, Application US/09629644A

Patent No. 6492345

GENERAL INFORMATION:

APPLICANT: Lex M. Cowsert

APPLICANT: Jacqueline Wyatt
                                                                                                                                                                                              Sequence 174, Application US/09487368A
Patent No. 6261840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 76.7%;
Best Local Similarity 88.2%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                         1 TTGGAGGGGGAGGTGGGG
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RESULT 7

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Sequence 45, Application US/09092077
Patent No. 6194142
GENERAL INFORMATION:
APPLICANT: Moncany, Maurice
APPLICANT: Montagnier, Luc
TITLE OF INVENTION: Nucleotide Sequences Derived From The
TITLE OF INVENTION: Genome Of Retroviruses Of The HIV-1, HIV-2 And SIV Type,
TITLE OF INVENTION: And Their Uses In Particular For The Amplification Of The
TITLE OF INVENTION: Of The Diseases Due To Those Viruses
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
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                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.7%; Score 13.8; DB 3;
88.2%; Pred. No. 1.7e+03;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/472,928
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/160,465
FILING DATE: 02-DEC-1993
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 8912371
FILING DATE: 20-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 8907354
FILING DATE: 06-FEB-1989
ATTOMNEY AGENT INFORMATION:
NAME: MSYSTEMETS FR 8907354
FILING DATE: 25-146
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0062-02000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               : 1300 I Street, N.W., Suite 700 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20005-3315

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ve.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/092,077

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 37, Application US/08242664
Patent No. 5571937
GENERAL INFORMATION:
APPLICANT: Watanabe, Kyoichi A.
APPLICANT: Ren, Wu-Yun
APPLICANT: Weil, Roger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 TGGAGGGGGAGGTGGGG 18
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 46
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Matches 15; Conserv
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Gaps
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                                                                                                                                                                                                                                                      Length 19;
                                                                                                                                                                                                                                                                                           .; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 37, Application PC/TUS9506379
GENERAL INFORMATION:
APPLICANT: Watanabe, Kyoichi A.
APPLICANT: Ren. Wu-Yun
APPLICANT: Weil, Roger
TITLE OF INVENTION: Complementary DNA and Toxins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSE: COOPER & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.4%; Score 13.4; DB 5;
93.3%; Pred. No. 2.5e+03;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                    Query Match 74.4%; Score 13.4; DB 1; Best Local Similarity 93.3%; Pred. No. 2.5e+03; Matches 14; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: New JOLA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch 1.44Mb

COMPUTER: IBM PC

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN PATA:

APPLICATION NUMBER: PCT/US95/06379

FILING DATE: May 13, 1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 44683-PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-278-0400

TELEPHONE: 212-391-0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
          TELECOMMUNICATION INFORMATION
                                                                                                                                                        , MOLECULE TYPE: DNA (genomic)
US-08-484-138-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                              TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GGAGGGGGAGGTGGG 17
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                                                                                                                                                                                                                                                                                                                                    3 GGAGGGGGAGGTGGG 17
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US-09-422-978-9409/c
                                                                                                                                               STRANDEDNESS
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PCT-US95-06379-37
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2.5e+03;
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Sequence 37, Application US/08484138

Settle No. 5652350

GENERAL INFORMATION:

APPLICANT: Watanabe, Kyoichi A.

APPLICANT: Weil, Roger

IITLE OF INVENTION:

CORRESPONDENCES: 43

CORRESPONDENCES: 43

CORRESPER: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.
TITLE OF INVENTION: Complementary DNA and Toxins NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/242,664
FILING DATE: May 12, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44683-Z/JPW/MJG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 74.4%; Score 13.4; D Similarity 93.3%; Pred. No. 2.5e 14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: IBM PC
COMPUTER: IBM PC
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,138
TTING DATE: June 7, 1995
                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4468:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-67-9550
TELEPHONE: 212-67-9550
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GGAGGGGGGGGGTGGG 17
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Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-08-484-138-37
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US-09-495-140-26

Sequence 26, Application US/09495140

Patent No. 6376182

GENERAL INFORMATION:
APPLICANT: CHAO, JULIE
APPLICANT: SONG, QING
TITLE OF INVENTION: OF ESSENTIAL HYPERTENSION
CURRENT APPLICATION NUMBER: 09/389,566
BARLIER FILING DATE: 1999-09-03
BARLIER FILING DATE: 1999-09-03
BARLIER FILING DATE: 1997-05-14
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
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CRGANISM: Artificial Sequence
FEATURE:
CHER INFORMATION: Description of Artificial Sequence:/No. 6376182e
CHER INFORMATION: synthetic construct
US-09-495-140-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

71.1%; Score 12.8; DB 2; Length 17;

Best Local Similarity 87.5%; Pred. No. 4.3e+03;

Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                             ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Michelson, A M, Orkin, S H.
TITLE: The 3' untranslated regions
TITLE: of the duplicated human alpha-globin genes are
JOURNAL: Cell
VOLUME: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; VOLUME: 22;
; PAGES: 371-377;
; DATE: 1980;
; RELEVANT RESIDUES IN SEQ ID NO: 127 :FROM 1 TO 17
US-08-173-489C-127
                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: alpha-1-globin gene (accession
DESCRIPTION: v00491) nucleotides 827 to 843
HYPOTHETICAL: no
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GGAGGGGGAGGTGGGG 18
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US-08-639-501-72
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LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-449 for SEQ 1544, in complemen
US-09-422-978-9409
                                                                       APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Chen, Daniel
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT APPLICATION NUMBER: US 09/298,850
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 9409
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 74.4%; Score 13.4; DB 4; Length 20; Best Local Similarity 93.3%; Pred. No. 2.5e+03; Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-08-173-489C-127/C
Sequence 127, Application US/08173489C
Sequence 127, Application US/08173489C
Sequence 127, Application US/08173489C
Sequence 127, Application US/08173489C
SEQUENCE SEQUENCE SEQUENCE ASSAY USING DNA TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 3.65
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC., STREET, SIO EAST 73RD STREET,
CONTRY: NEW YORK
COUNTRY: USA
ZIP: NEW YORK
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: BM PC/XT/AT
COMPUTER: DATA:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: DATA:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: USA
ZIP: MCDILCATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
COLASSITCATION NUMBER: US/08/173,489C
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TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 127:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
Sequence 9409, Application US/09422978 Patent No. 6537751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TIGGAGGGGGAGGIG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo Sapiens
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APPLICANT: Tavtigian, Sean V.
APPLICANT: Kamb, Alexander
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Couch, Fergus
APPLICANT: Rommens, Johanna
APPLICANT: Weber, Barbara
TITLE OF INVENTION: Chromosome 13-Linked Breast Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1001
CITY: Washington
STATE: DC
COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/044,946
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/576,559
FILING DATE: 21-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/575,359
FILING DATE: 20-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/573,779
FILING DATE: 18-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/639,501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                APPLICANT: Tavtigian, Sean V.
APPLICANT: Ramb, Alexander
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Couch, Fergus
APPLICANT: Rommens, Johanna
APPLICANT: Weber, Barbara
TITLE OF INVENTION: Chromosome 13-Linked Breast Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match, 71.1%; Score 12.8; DB 2; Length 18; Best Local Similarity 87.5%; Pred. No. 4.3e+03; Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639,501
FILING DATE: 29-APR-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/576,559
FILING DATE: 11-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/575,359
FILING DATE: 20-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/575,359
FILING DATE: 18-DEC-1995
FILING DATE: 18-DEC-1995
FILING DATE: 18-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: That Information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-116802-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
Sequence 72, Application US/08639501
Patent No. 5837492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 7;
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORIGINAL SOURCE
) ORGANISM: HOI
US-08-639-501-72
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                                                                            Length 18;
                                                                                                       2; Indels
                                                                          Score 12.8; DB 3;
Pred. No. 4.3e+03;
0; Mismatches 2;
                                                                                                                                                                                                          Search completed: October 27, 2003, 14:03:35 Job time: 41.3143 secs
                                                                          Query Match 71.1%;
Best Local Similarity 87.5%;
Matches 14; Conservative (
                                                                                                                                    1 TTGGAGGGGGAGGTGG 16
ANTI-SENDE.
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                1 Tradadadacadarad
                                              US-09-044-946-72
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RESULT 15 US-09-044-946-72 ; Sequence 72, Application US/09044946 ; Patent No. 6033857

TTGGAGGGGGAGGTGG 16 rridgadadacaddrad 16

ΩD 8

18 base pairs nucleic acid

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October 27, 2003, 11:25:34; Search time 387.943 Seconds (without alignments) 124:432 Million cell updates/sec
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1: cgn2 6/ptodata/1/pubbna/USO7 PUBCOMB.seq:*

2: cgn2 6/ptodata/1/pubbna/DSO6 NEW PUB.seq:*

3: cgn2 6/ptodata/1/pubbna/USO6 NEW PUB.seq:*

4: cgn2 6/ptodata/1/pubpna/USO6 PUBCOMB.seq:*

5: cgn2 6/ptodata/1/pubpna/USO7 NEW PUB.seq:*

6: cgn2 6/ptodata/1/pubpna/USO8 NEW PUB.seq:*

7: cgn2 6/ptodata/1/pubpna/USO8 PUBCOMB.seq:*

8: cgn2 6/ptodata/1/pubpna/USO9 PUBCOMB.seq:*

10: cgn2 6/ptodata/1/pubpna/USO9 PUBCOMB.seq:*

11: cgn2 6/ptodata/1/pubpna/USO9 NEW PUB.seq:*

12: cgn2 6/ptodata/1/pubpna/USO9 NEW PUB.seq:*

13: cgn2 6/ptodata/1/pubpna/USO9 NEW PUB.seq:*

14: cgn2 6/ptodata/1/pubpna/USO9 NEW PUB.seq:*

15: cgn2 6/ptodata/1/pubpna/USO9 NEW PUB.seq:*

16: cgn2 6/ptodata/1/pubpna/USO8 NEW PUB.seq:*

17: cgn2 6/ptodata/1/pubpna/USO8 NEW PUB.seq:*

16: cgn2 6/ptodata/1/pubpna/USO8 NEW PUB.seq:*

17: cgn2 6/ptodata/1/pubpna/USO8 NEW PUB.seq:*

16: cgn2 6/ptodata/1/pubpna/USO8 NEW PUB.seq:*

17: cgn2 6/ptodata/1/pubpna/USO8 NEW PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1792395 seqs, 1340900451 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                      US-09-331-204A-8
18
1 ttggaggggaggtgggg 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0 Maximum DB seq length: 22
                                                                                                                                                                                                                                                                                                                                                      Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                        Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 30, Appl	_	3.4	• •	Sequence 1936, Ap		67,	28, 19		Sequence 45, Appl	894,	26,	26,	175,	32,	Sequence 34, Appl
QI	US-10-303-109A-30	US-09-854-883-174	US-10-061-201-1934	US-10-061-201-1935	US-10-061-201-1936	US-10-010-920-67	US-10-008-721-67	US-09-828-034-28	US-10-233-032A-22	US-09-780-533A-45	US-09-780-533A-894	US-10-059-877-26	US-10-059-888-26	US-09-854-883-175	US-09-952-464A-32	US-10-060-301-34
DB	12	ഗ	12	12	12	74	14	מ	12	17	11	12	14	σ	11	13
Length	17	50	17	17	17	6 H	19	21	70	17	17	17	17	20	20	20
% Query Match	80.0	76.7	74.4	74.4	74.4	74.4	74.4	73.3	72.2	71.1	71.1	71.1	71.1	71.1	71.1	71.1
Score	14.4	13.8	13.4	13.4	13.4	13.4	13.4	13.2	13	12.8	12.8	12.8	12.8	12.8	12.8	12.8
Result No.	C	7	ო ს	Ω	Ω Ω	w	7	ω υ	σι	c 10	c 11	12	13	14	c 15	c 16

RESULT 2
US-09-854-883-174
; Sequence 174, Application US/09854883
; Patent No. US20020055479A1
; APPLICANT: LIFORMATION:
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia

12 4 68 9 17 12 118-10-238-700.3257 Semience 326.	1/ 12.4 60.9 1/ 12 US-10-250-/00-523/ Sequenc 18 12.4 68.9 1/ 12 US-10-061-201-1933 Sequenc	19 12.4 68.9 1/ 12 US-10-051-201-193/ Sequence 193	21 12.2 67.8 17 9 US-09-866-108-1256 Sequence 1256	2 12.2 67.8 17 11 US-09-930-423-1590 Sequence 159	12.2 67.8 17 12 to - 19-745-23/A-1590 Sequence 159	4 12.5 67.8 17 12 US-10-001-201-1950 Sequence 195	50 17 2 67 8 20 17 112-10-10132-48333 SEQUENTICE 603.	11 11 11 11 11 11 11 11 11 11 11 11 11		8 12 66./ 16 12 US-10-U84-839-25/U SEQUENCE 25/ 9 11 8 65 6 16 12 NS-10-069-877-23	7 11.6 60.0 16 17 115.10.009.20 0.00.000.00 0.00.000.00 0.00.000.000	30 11.8 69.5	31 II. 8 69.6 II. II US-CO-1800-1933A-2034 Sequence 894	34 II.8 65:6 I. US-04-/80-533A-895 Sequence 895	1 11 0S-09-930-423-1591 Sequence 159	4 11.8 65.6 17 11 US-09-740-332-1833 Sequence 183.	11.8 65.6 1/ 12 US-09-/45-23/A-1591 Sequence 159	6 11.8 65.6 17 12 US-09-817-879-1833 Sequence 1833	7 11.8 65.6 18 14 US-10-265-689-40 Sequence 40,	8 11.8 65.6 19 12 US-10-205-309-49 Sequence 49,	39 11.8 65.6 19 12 US-10-205-309-374 Sequence 374	40 11.8 65.6 20 10 US-09-874-162A-22 Sequence 22,	41 11.8 65.6 20 11 US-09-948-002-30 Sequence 30,	42 11.8 65.6 20 12 US-10-024-369-5 Sequence 5, 3	43 11.8 65.6 20 12 US-10-024-369-33 Sequence 33,	44 11.8 65.6 21 11 US-09-932-300-10 Sequence 10.	45 11.8 65.6 21 11 US-09-932-300-24 Sequence 24,	ALIGNMENTS
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us-09-331-204a-8.szlm22.rnpb

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Query Match 74.4%; Score 13.4; DB 12; Length 17; Best Local Similarity 93.3%; Pred. No. 1.7e+04; Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1936/C

Sequence 1936, Application US/10061201

Publication No. U520030166229A1

GENERAL INFORMATION:

APPLICANT: Shannon, Mark

TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1

FILE REFERENCE: PB0178

CURRENT FILING DATE: 2002-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                               Sequence 1935, Application US/10061201

Bublication No. US20030166229A1

GENERAL INFORMATION:

APPLICANT: Shannon, Mark

TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN I
FILE REFERENCE: PB0178

CURRENT APPLICATION NUMBER: US/10/061,201

CURRENT APPLICATION NUMBER: US/10/061,201

CURRENT APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GAGGGGGAGGTGGGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 GAGGGGGAGGAGGGG 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-061-201-1936/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
APPLICANT: Madeline M. Butler
APPLICANT: Robert McKay
TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
FILE REFERENCE: ISPH-0576
CURRENT APPLICATION NUMBER: US/09/854,883
CURRENT APPLICATION NUMBER: US 09/629,644
PRIOR APPLICATION NUMBER: US 09/629,644
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 389
SEQ ID NO 174
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 76.7%; Score 13.8; DB 9; Length 20; Best Local Similarity 88.2%; Pred. No. 1.1e+04; Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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93.3%; Pred. No. 1.7e+04;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Shannon, Mark

TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PB0178

CURRENT APPLICATION NUMBER: US/10/061,201

CURRENT FILING DATE: 2002-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Antisense Oligonucleotide
US-09-854-883-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1934, Application US/10061201
Publication No. US20030166229A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TGGAGGGGGAGGTGGGG 18
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; ORGANISM: Homo sapiens
US-10-061-201-1934
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Matches 14; Conserv
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Matches

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Sequence 22, Application US/10233032A

Sequence 22, Application US/10233032A

Publication No. US20030157704A1

GENERAL INFORMATION:

APPLICANT: Roninson, Igor

APPLICANT: Chang, Bey-Dih

TITLE OF INVENTION: REAGENTS AND METHODS FOR IDENTIFYING AND MODULATING

TITLE OF INVENTION: REPRESSION OF GENES REGULATED BY CDK INHIBITORS

TITLE OF INVENTION: REPRESSION OF GENES REGULATED BY CDK INHIBITORS

TITLE OF INVENTION: BY 126-A

CURRENT APPLICATION NUMBER: US/10/233,032A

CURRENT FILING DATE: 2003-02-12

PRIOR FILING DATE: 2002-05-21

PRIOR PRIOR FILING DATE: 2002-02-01

NUMBER OF SEQ ID NOS: 84

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 22

LENGTH: 20
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                                     ; OTHER INFORMATION: Description of Artificial Sequence: Primer ON-DHFR-F1 US-10-008-721-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
CRGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-28
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                                                                                                             Query Match 74.4%; Score 13.4; DB 14; Best Local Similarity 93.3%; Pred. No. 1.7e+04; Matches 14; Conservative 0; Mismatches 1;
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Pred. No. 1.9e+04;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                               Sequence 28, Application US/09828034

| Sequence 28, Application US/09828034
| Patent No. US20020064771A1
| GENERAL INFORMATION:
| APPLICANT: Zhong, Weidong
| APPLICANT: Hong, Zhi
| CURRENT APPLICATION NUMBER: US/09/828,034
| CURRENT APPLICATION NUMBER: U.S. 60/195,852
| PRIOR APPLICATION NUMBER: U.S. 60/195,852
| PRIOR FILING DATE: 2000-04-06
| NUMBER OF SEQ ID NOS: 33
| SOFTWARE: PatentIn Ver. 2.1
| SEQ ID NO 28
| LENGTH: 21
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Best Local Similarity 83.3%;
Matches 15; Conservative (
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US-09-828-034-28/c
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US-10-233-032A-22
              FEATURE:
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TITLE OF INVENTION: Alternatively spliced polk nucleotide and amino acid sequences
TITLE OF INVENTION: and methods for using
TITLE OF INVENTION: and methods for using
FILE REFERENCE: 98,723-E3
CURRENT APPLICATION NUMBER: US/10/010,920
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/254,649
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 67
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Publication No. US20030082745A1

GENERAL INFORMATION:
APPLICANT: Saus, Juan
TITLE OF INVENTION:
FILE REFERENCE: 98,723-E1
CURRENT APPLICATION NUMBER: US/10/008,721

CURRENT FILING DATE: 2000-12-07

PRIOR FILING DATE: 2000-12-08

NUMBER OF SEQ ID NOS: 102

SOFTWARE: Fatentin Ver. 2.0
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Pred. No. 1.7e+04;
0; Mismatches 1;
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PRIOR APPLICATION NUMBER: PCT/US01/00670;
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR PLICATION NUMBER: US 60/328,205
PRIOR PLING DATE: 2001-10-10
NUMBER OS DI NOS: 4162
SOFTWARE: Aeomica Sequence Listing Engine;
SEQ ID NO 1936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 67, Application US/10010920 Publication No. US20030027165A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        Query Match 74.4%;
Best Local Similarity 93.3%;
Matches 14; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 GAGGGGGAGGAGGGG 1
                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-10-061-201-1936
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US-10-010-920-67
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US-10-008-721-67
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FUBLICATION NO. US20030157490A1
GENERAL INFORMATION:
FAPLICANT: CHAO, ULE
APPLICANT: CHAO, ULE
APPLICANT: CHAO, ULE
APPLICANT: SONG, QING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING
TITLE OF INVENTION: HYPERTENSION
TITLE OF INVENTION: HYPERTENSION
FILE REFERENCE: 19113.008102
CURRENT PAPLICATION UNMBER: 09/495,140
FRIOR PELING DATE: 2000-01-31
FRIOR PILING DATE: 1999-09-03
FRIOR FILING DATE: 1999-09-03
FRIOR FILING DATE: 1997-05-14
FRIOR FILING DATE: 1997-05-14
SOFTWARE: FASEUSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 17
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GENERAL INFORMATION:
APPLICANT: CHAO, LEE
APPLICANT: CHAO, JULE
APPLICANT: CHAO, JULE
APPLICANT: SONG, QING
TITLE OF INVENTION: HETHODS AND COMPOSITIONS FOR CORRELATING
TITLE OF INVENTION: HYPERTERSION
TITLE OF INVENTION: HYPERTERSION
FILE REFERENCE: 19113.008102
CURRENT APPLICATION NUMBER: US/10/059,888
CURRENT FILING DATE: 2002-01-29
CURRENT FILING DATE: 2000-01-31
PRIOR FILING DATE: 1999-09-03
PRIOR PELICATION NUMBER: 09/495,140
PRIOR PILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1997-05-14
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence:/No. US20030157490Ale = CHER INFORMATION: synthetic construct
US-10-059-877-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 71.1%; Score 12.8; DB 12; Best Local Similarity 87.5%; Pred. No. 2.9e+04; Matches 14; Conservative 0; Mismatches 2;
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                                                                                                                             ; Sequence 26, Application US/10059877; Publication No. US20030157490A1
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
17 GGAGGGGGAGGCCGGG
                                                                          RESULT 12
US-10-059-877-26
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APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Hackerli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MEHBOO, 878-A (400/011)
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOTTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Chowrira, Bharat
APPLICANT: Chowrira, Bharat
APPLICANT: Haeberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBHB00,878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: Patentin version 3.0
SECTION 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.1%; Score 12.8; DB 11; Length 17; 87.5%; Pred. No. 2.9e+04; tive 0; Mismatches 2; Indels
                      Score 13; DB 12; Length 20;
Pred. No. 2.3e+04;
0; Mismatches 0; Indels
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; Sequence 894, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme_Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                             RESULT 10
US-09-780-533A-45/c
; Sequence 45, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
                   Query Match
72.2%; Sc
Best Local Similarity 100.0%; P
Matches 13; Conservative 0;
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Best Local Similarity 87.5
Matches 14; Conservative
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Matches 14, Conservative
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CORGANISM: Homo sapiens
US-09-780-533A-894
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ORGANISM: Homo sapiens
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APPLICANT: Lex M. Cowsert
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Brett P. Monia
APPLICANT: Madeline M. Butler
APPLICANT: Madeline M. Butler
APPLICANT: Madeline M. Butler
APPLICANT: Robert McKay
TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
FILE REFERENCE: 1SPH-0576
CURRENT APPLICATION NUMBER: US/09/854,883
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 09/629,644
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 09/487,368
PRIOR FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 389
SEQ ID NO 175
LENGTH: 20
      Score 12.8; DB 14; Length 17; Pred. No. 2.9e+04; 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENEKAL INFORMATION:
APPLICANT: Stone, Edwin M.
APPLICANT: Sheffield, Val C.
APPLICANT: Sheffield, Val C.
APPLICANT: Sheffield, Val C.
APPLICANT: Alward, Wallace L.M.
APPLICANT: Fingert, John
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
FILE REFERENCE: 21087.0017U11
CURRENT APPLICATION NUMBER: US/09/952,464A
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 09/461,542
PRIOR FILING DATE: 1999-12-18
PRIOR FILING DATE: 1999-08-04
PRIOR FILING DATE: 1999-08-04
PRIOR FILING DATE: 1999-08-04
PRIOR FILING DATE: 1999-08-04
PRIOR FILING DATE: 1997-03-21
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 71.1%; Score 12.8; DB 9; Best Local Similarity 87.5%; Pred. No. 2.8e+04; Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Antisense Oligonucleotide US-09-854-883-175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 32, Application US/09952464A Publication No. US20030077587A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    Sequence 175, Application US/09854883
Patent No. US20020055479A1
Query Match
Best Local Similarity 87.5%; Pr
Matches 14; Conservative 0;
                                                                                                       3 GGAGGGGAGGTGGGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TGGAGGGGGAGGTGGG 17
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Title: Perfect

Run on:

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October 27, 2003, 10:32:35; Search time 2356.29 Seconds (without alignments) 253.343 Million cell updates/sec
                                                                                                                                                                                                                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                       33363688 segs, 16581889874 residues
                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                               - nucleic search, using sw model
                                                                                                              IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                              ttggaggggaggtgggg 18
                                                                              US-09-331-204A-8
18
1 ttggagggggaggtg
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Maximum DB seq length: 22
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                                                                                                              Scoring table:
                               OM nucleic
                                                                                                Sequence:
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1/pna/US100B_COMB.seq:*
1/pna/US101A_COMB.seq:*
1/pna/US101B_COMB.seq:*
1/pna/US101B_COMB.seq:*
1/pna/US103A_COMB.seq:*
1/pna/US104A_COMB.seq:*
1/pna/US6001_COMB.seq:*
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1/pna/US6001_COMB.seq:*
1/pna/US6001_COMB.seq:*
1/pna/US6001_COMB.seq:*
1/pna/US6001_COMB.seq:*
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/pna/US6025
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 5, Appli	Sequence 8, Appli	Sequence 3, Appli	Sequence 1, Appli
SUMMARIES		US-09-331-204-5	18 19 US-09-331-204A-8	US-08-387-041A-3	19 US-09-331-204-1
	DB	19	64	00	19
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d	Query Match	9 100.0	100.0	91.1	91.1
	Score		18	16.4	16.4
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Gaps

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Indels

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18; Conservative

Matches

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1 TTGGAGGGGAGGTGGGG 18

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Sequence 17, Appl
Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 79, Appli
Sequence 38, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 147, Appl
Sequence 1706, Appl
Sequence 174, Appl
Sequence 1856, Appl
Sequence 1814, Appl
Sequence 1816, A
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Sequence 5, Application US/09331204

GENERAL INFORMATION:

APPLICANT: Tam, Robert

TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN

TITLE OF INVENTION: IMMUNE RESPONSE

CURRENT APPLICATION NUMBER: US/09/331,204

CURRENT APPLICATION NUMBER: PCT/US97/23927

PRIOR APPLICATION NUMBER: PCT/US97/23927

PRIOR APPLICATION NUMBER: PCT/US97/23927

PRIOR APPLICATION NUMBER: PCT/US97/23927

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: or polymer of ribonucleic acid or decoxyribonucleic

OTHER INFORMATION: acid. This term includes oligomers consisting of

OTHER INFORMATION: naturally occurring bases, sugars and intersugar (
US-09-331-204-5
US-09-331-204A-4

US-09-331-204A-7

US-09-786-436-17

US-09-786-436-17

US-09-331-204-4

US-09-331-204-4

US-09-331-204-4

US-09-331-204-4

US-09-331-204-4

US-09-331-204-4

US-09-331-204-4

US-09-331-204-4

US-09-331-204A-6

US-10-310-188-47426

US-10-310-188-47426

US-10-310-188-47426

US-10-310-188-47426

US-10-310-188-47426

US-10-310-188-47426

US-10-302-37764-30

US-10-302-37764-30

US-10-302-817A-51

US-10-303-109A-30

US-10-303-109A-30

US-10-303-109A-30

US-10-303-109A-30

US-10-303-109A-30

US-10-310-188-26651

PCT-US01-0109-174

US-09-670-105-45

US-10-366-090-456565

US-10-36-091-1935

US-10-310-188-51847

US-00-328-205-1935

US-10-328-205-1935

US-10-36-090-46765
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100.0%; Score 18; DB 19; Length 18; 100.0%; Pred. No. 5.1e+03;

Query Match Best Local Similarity

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RESULT 2
US-09-331-204A-8

i Sequence 8, Application US/09331204A

j Sequence 8, Application US/09331204A

j GENERAL INFORMATION:

APPLICANT: Tan, Robert

TITLE OF INVENTION:

FILE REPERENCE: 216/013-051

CURRENT APPLICATION NUMBER: US/09/331,204A

CURRENT FILING DATE: 1999-08-20

PRIOR APPLICATION NUMBER: PT/US97/23927

PRIOR APPLICATION NUMBER: PT/US97/23927

PRIOR APPLICATION NUMBER: 1997-12-19

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.0

SEQ ID NO 8

LENGTH: 18

LENGTH: 18
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GENERAL INFORMATION:

APPLICATION

TITLE OF INVENTION:

METHODS AND COMPOSITIONS FOR REGULATION

TITLE OF INVENTION:

MUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

CONTRY:

New York

COUNTRY:

New York

COUNTRY:

MEDIUM TYPE:

MEDIUM TYPE:

MEDIUM TYPE:

COMPUTER:

MEDIUM TYPE:

MEDIUM
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LENGTH: 18 Daccid
TVPE: nucleic acid
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US-08-387-041A-3
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APPLICANT: ICN Pharmaceuticals, Inc.
APPLICANT: Tam, Robert
TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Rest
FILE REFERENCE: 216/013-US1
CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR APPLICATION NUMBER: PCT/US97/23927
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
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APPLICANT: Lipford, Grayson
APPLICANT: Lipford, Grayson
APPLICANT: Heeg, Klaus
TITLE OF INVENTION: G-Motif Oligonucleotides and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: C1041/7010 (AWS)
CURRENT APPLICATION NUMBER: US/09/786,436
CURRENT FILING DATE: 2001-03-02
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APPLICANT: Lipford, Grayson
APPLICANT: Heeg, Klaus
TITLE OF INVENTION: G-Motif Oligonucleotides and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.1%; Score 16.4; DB 33; 94.4%; Pred. No. 2.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 91.1%; Score 16.4; DB 19; Best Local Similarity 94.4%; Pred. No. 2.1e+04; Matches 17; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Synthetic oligonucleotide US-09-786-436-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/EP99/06502
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                Sequence 7, Application US/09331204A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: synthetic construct US-09-331-204A-7
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Best Local Similarity 94.4*
Matches 17; Conservative
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LENGTH: 18
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APPLICANT: Tam, Robert
TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Respt
FILE REFERENCE: 216/013-US1
CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 18
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TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
TITLE OF INVENTION: IMMUNE RESPONSE
FILE REFERENCE: ICNSequence
CURRENT APPLICATION NUMBER: US/09/331,204
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: Description of Artificial Sequence: An oligomer; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic; OTHER INFORMATION: acid including oligomers consisting of naturally; OTHER INFORMATION: occurring bases, sugars and intersugar US-09-331-204-1
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Pred. No. 2.1e+04;
0; Mismatches 1;
                                                                                            Score 16.4; DB 8;
Pred. No. 2.1e+04;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09331204A GENERAL INFORMATION:
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GENERAL INFORMATION:
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TOPOLOGY: unknown
MECULE TYPE: DNA (genomic)
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                                                                                          Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
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Best Local Similarity
Matches 17; Conserv
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                     ; MOLECULE TY|
US-08-387-041A-3
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ENGTH: 18
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US-09-331-204-1
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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TOPOLOGY: ur
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Sequence 4, Application US/09331204

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN TITLE OF INVENTION: IMMUNE RESPONSE
FILE REFERENCE: ICNSequence
CURRENT APPLICATION NUMBER: US/09/331,204

CURRENT APPLICATION NUMBER: PCT/US97/23927

PRIOR APPLICATION NUMBER: PCT/US97/23927

PRIOR FILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: An oligomer

OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic;

OTHER INFORMATION: acid. This term includes oligomers consisting of;

OTHER INFORMATION: naturally occurring bases, sugars and intersugar (US-09-331-204-4
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GENERAL INFORMATION:
APPLICANT: Tam, Robert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION
TITLE OF INVENTION: OF CD28 EXPRESSION
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 91.1%; Score 16.4; DB 19; Length 19; Best Local Similarity 94.4%; Pred. No. 2.1e+04; Matches 17; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Length 18;
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                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Synthetic oligonucleotide US-09-786-436-42
TITLE OF INVENTION: Thereof;
FILE REFERENCE: C1041/7010 (AWS);
CURRENT APPLICATION NUMBER: US/09/786,436
CURRENT FILING DATE: 2001-03-02;
PRIOR APPLICATION NUMBER: PCT/EP99/06502;
PRIOR FILING DATE: 1999-09-03;
NUMBER OF SEQ ID NOS: 42;
SOFTWARE: FastSEQ for Windows Version 3.0;
SEQ ID NO 42
LENGTH: 18
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ORGANISM: Artificial Sequence
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US-08-387-041A-4
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Sequence 6, Application US/09331204
; Sequence 6, Application US/09331204
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
; TITLE OF INVENTION: IMMUNE RESPONSE
; FILE REFERENCE: ICNS equence
; CURRENT APPLICATION NUMBER: US/09/331,204
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR PFLING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.1%; Score 16.4; DB 8; Length 21; 94.4%; Pred. No. 2.1e+04; ive 0; Mismatches 1; Indels
COMPUTER READABLE FOWM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,041A
FILING DATE: 02-FEB-1995
CLASSIFICATION: S14
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8250-011
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-984-3694
TELEFAX: 415-984-3694
TELEFAX: 415-984-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TUDENT: NUMBER: AUSPERISTICS:
LENGTH: 21 base pairs
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US-09-331-204A-6
; Sequence 6, Application US/09331204A
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Best Local Similarity
Matches 17; Conserv
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Gaps

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RESULT 15
US-09-979-666B-79
Sequence 79, Application US/09979666B
GENERAL INFORMATION:
APPLICANT: TACHAS, GEORGE
TITLE OF INVENTION: INHIBITION OF GASTRIC ACID PRODUCTION AND/OR SECRETION
FILE REFERENCE: 47-162
FURRENT APPLICATION NUMBER: US/09/979,666B
CURRENT APPLICATION NUMBER: US/09/979,666B
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 79
LENGTH: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
OTHER INFORMATION: Synthetic antisense oligonuclectide, can be
OTHER INFORMATION: RNA, DNA or chimera
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Syntheti
OTHER INFORMATION: antisense oligonuclectide, can be RNA, DNA
COTHER INFORMATION: or chimera
US-09-979-6668-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.2%; Score 14.8; DB 42; Length 22; 81.2%; Pred. No. 8.3e+04; tive 3; Mismatches 0; Indels (
            Indels
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0
          Mismatches
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Best Local Similarity 81.2
Matches 13; Conservative
          15; Conservative
          Matches
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GENERAL INFORMATION:
APPLICANT: ICN Pharmaceuticals, Inc.
APPLICANT: Tam, Robert
TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Response Elle Reference: 216/013-US1
CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT APPLICATION NUMBER: PCT/US97/23927
PRIOR FILING DATE: 1997-08-20
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 47426, Application US/10310188
GENERAL INFORMATION:
APPLICANT: RosettaGemonics
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
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APPLICANT: ROSELLEGEMONICS
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT APPLICATION NUMBER: US/10/310,188
SOFTWARE: Patentin version 3.1
SEQ ID NO 38927
LENGTH: 18
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Pred. No. 6.9e+04;
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Pred. No. 2.1e
0; Mismatches
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100.0%;
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; ORGANISM: synthetic construct
US-09-331-204A-6
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11 Similarity 94.4%;
17; Conservative
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Best Local Similarity 94.1
Matches 16; Conservative
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; ORGANISM: Homo sapiens
US-10-310-188-47426
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Best Local Similarity
Matches 17; Conserv
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Best Local Similarity
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US-10-310-188-38927
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US-10-310-188-38927
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Gaps

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October 27, 2003, 11:09:34; Search time 307.029 Seconds (without alignments) 97.777 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                 2231628 seqs, 833900706 residues
                                                                             - nucleic search, using sw model
                                                                                                                                                                                           US-09-331-204A-8
18
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                           Title:
Perfect score:
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Post-processing: Minimum Match 00% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 22

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2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:

4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:

5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:

6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:

7: /cgn2_6/ptodata/1/pna/US00_NEW_COMB.seq:

6: /cgn2_6/ptodata/1/pna/US00_NEW_COMB.seq:

7: /cgn2_6/ptodata/1/pna/US00_NEW_COMB.seq: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	7 4 7	e 3892	e 1166,	e 47706,	e 26651	e 174,	51847	6227,	25860	3897	equence 51829	36515	equence 18159	equence 25810	64492	equence 64684	41825	18366	39032	equence 14773	14816	38911	equence 622	e 9731,	18298,	3900
ID	-38216-4742	-US02-38216-389	-11	-US02-38216-4770	-US02-38216-26	US-09-629-644A-174	-518	38	-2586	PCT-US02-38216-38977	6-5182	6-3651	PCT-US02-38216-18159	6-2581	6-644	PCT-US02-38216-64684	-4182	PCT-US02-38216-18366	PCT-US02-38216-39032	02-38	PCT-US02-38216-14816		16-622	-38216-97	PCT-US02-38216-18298	PCT-US02-38216-39006
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% Query Match	85.6	83.3	80.0	80.0	76.7	76.7	76.7	74.4	74.4	74.4	74.4	73.3	73.3	72.2	72.2	72.2	72.2	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1
Score	15.4	15	14.4	14.4	13.8	13.8	13.8		13.4	13.4	m	13.2	ო	13	13	13	13	•	4	ų.	ά.	ď	•	ά.	ζ.	12.8
Result No.	:	7	m	4	ω ω	vo	۲	ω υ	0	10	11	12	13	H	c 15	Н	17	18	٦ 9	20	21	22	c 23	24	25	26

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Sequence Sequence	Sequence	Seguence	Seguence	w	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Seguence	Seguence	Sequence	Sequence
PCT-US02-38216-39031 PCT-US02-38216-39102	-US02-3	6-5184	216-5827	09-9	PCT-US02-38216-61077	6-6110	6-7281	6-1077	PCT-US02-38216-18422	216-3891	16-3894	-4697	2-38216-148	PCT-US02-38216-18227	PCT-US02-38216-18520	PCT-US02-38216-26672	16-4183
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ALIGNMENTS

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Sequence 47426, Application PC/TUS0238216

Sequence 47426, Application PC/TUS0238216

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002

CURRENT APPLICATION NUMBER: PCT/US02/38216

CURRENT APPLICATION NUMBER: PCT/US02/38216

CURRENT FILING DATE: 2002-11-12

CURRENT FILING DATE: 2002-11-12

SOFTWARE: Patentin version 3.2

SEQ ID NO 47426

LENGTH: 19

TYPE: DNA

ORGANISM: Homo sapiens

PCT-US02-38216-47426
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PCT-US02-38216-38927
; Sequence 38927, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 38927
; LENGTH: 18
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CRGANISM: Homo sapiens
PCT-US02-38216-38927
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Gaps

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PCT-USIGNATION:
Sequence 26651, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT PAPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
LENGTH: 19
Gaps
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US-09-629-644A-174
; Sequence 174, Application US/09629644A
; GENERAL INFORMATION:
    APPLICANT: Lex M. Cowsert
    APPLICANT: Jacqueline Wyatt
    APPLICANT: Brett P. Monia
    APPLICANT: Brett P. Monia
    APPLICANT: Robert McKay
    TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
    TITLE OF INVENTION: ANTISENSE WOOULATION OF PTP1B EXPRESSION
    FILE REFERENCE: ISPH-0478
    CURRENT APPLICATION NUMBER: US/09/629,644A
    CURRENT FILING DATE: 2000-07-31
    PRIOR APPLICATION NUMBER: US 09/487,368
    PRIOR FILING DATE: 2000-01-18
    NUMBER OF SEQ 1D NOS: 242
; SEQ 1D NO 174
; LENGTH: 20
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Best Local Similarity 88.2%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels
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76.7%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels
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, CTHER INFORMATION: Antisense Oligonucleotide US-09-629-644A-174
  Mismatches
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PCT-US02-38216-51847
; Sequence 51847, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
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                                                                  3 GGAGGGGGAGGTGGGG 18
       15; Conservative
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ORGANISM: Homo sapiens
PCT-US02-38216-26651
          Matches
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SEQUENCE 1166, Application PC/TUS0326780
SEGURAL INFORMATION: HUMAN POLYTEPTICS, INC.
APPLICANT; FUTERIME THERAPEUTICS, INC.
TITLE OF INVENTION: HUMAN POLYTEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF TITLE OF INVENTION: HERE NO.
TITLE OF INVENTION: HUMAN POLYTEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF TITLE OF INVENTION: HERE NO.
CURRENT APPLICATION NUMBER: 60/406,519
PRIOR APPLICATION NUMBER: 60/406,579
PRIOR PELLING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,566
PRIOR PELLING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,566
PRIOR APPLICATION NUMBER: 60/406,666
PRIOR APPLICATION NUMBE
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PCT-US02-38216-47706

Sequence 47706, Application PC/TUS0238216

GENERAL INFORMATION:

APPLICANT: Rosetta Genomics LTD

TITLE OF INVENTION: GENES AND USES THEREOF

FILE REFERENCE: 55002

CURRENT APPLICATION NUMBER: PCT/US02/38216

CURRENT FILING DATE: 2002-11-12

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: Patentin version 3.2

LENGTH: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 80.0%; Score 14.4; DB 1; Length 21; Best Local Similarity 93.8%; Pred. No. 1.3e+04; Matches 15; Conservative 0; Mismatches 1; Indels
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93.8%;
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          3 GGAGGGGAGGTGGG 17
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CRGANISM: Homo sapiens
PCT-US02-38216-47706
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Best Local Similarity
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PCT-US02-38216-36515

PCT-US02-38216-36515

Sequence 36515, Application PC/TUS0238216

GENERAL INFORMATION:

APPLICANT: Rosetta Genomics LTD

TITLE OF INVENTION: GENES AND USES THEREOF

TITLE OF INVENTION: GENES AND USES THEREOF

FILE REFERENCE: 55002

CURRENT APPLICATION NUMBER: PCT/US02/38216

CURRENT FILING DATE: 2002-11-12

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: PatentIn version 3.2

SEQ ID NO 36515

LENGTH: 20
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; Sequence 51829, Application PC/TUS0238216
; GENERAL INFORMATION:
    APPLICANT: ROSELTA GENOMICS LTD
; TITLE OF INVENTION: BENES AND USES THEREOF
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.2
; SOFTWARE: Patentin version 3.2
; SOFTWARE: OS 1829
                                                                         RESULT 10
PCT-US02-38216-38977
; Sequence 38977, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: GENES AND USES THEREOF
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT PLING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 38977
; LENGTH: 18
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24.4%; Score 13.4; DB 1; Length 21;

Best Local Similarity 93.3%; Pred. No. 3e+04;

Matches 14; Conservative 0; Mismatches 1; Indels
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  18 GGTGGGGGAGGTGGG
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) ORGANISM: Homo sapiens
pCT-USO2-38216-51829
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; ORGANISM: Homo sapiens
PCT-US02-38216-38977
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; Sequence 25860, Application PC/TUS0238216
; GENERAL INFORMATION:
    APPLICANT: Rosetta Genomics LTD
    TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
    TITLE OF INVENTION: GENES AND USES THEREOF
    FILE REFERENCE: 55002
    CURRENT APPLICATION NUMBER: PCT/US02/38216
    CURRENT PILING DATE: 2002-11-12
    NUMBER OF SEQ ID NOS: 86841
    SOFTWARE: Patentin version 3.2
; SEQ ID NO 25860
    LENGTH: 18
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FCT-COS02-38216-6227/C

FCT-COS02-38216-6227, Application PC/TUS0238216

GENERAL INFORMATION:

APPLICANT: Rosetta Genomics LTD

TITLE OF INVENTION: GENES AND USES THEREOF

TITLE OF INVENTION: GENES AND USES THEREOF

FILE REFERENCE: 55002

CURRENT APPLICATION NUMBER: PCT/US02/38216

CURRENT APPLICATION NUMBER: PCT/US02/38216

CURRENT FILING DATE: 2002-11-12

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: Patentin version 3.2

SEQ ID NO 6227
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY TITLE OF INVENTION: GENES AND USES THEREOF FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 51847
LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                         Score 13.8; DB 1; Length 21; Pred. No. 2.2e+04; 0; Mismatches 2; Indels
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Best Local Similarity 93.3%;
Matches 14; Conservative C
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Best Local Similarity 88.2%;
Matches 15; Conservative (
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Best Local Similarity 93.3
Matches 14, Conservative
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ORGANISM: Homo sapiens
PCT-US02-38216-25860
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
PCT-US02-38216-51847
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Search completed: October 27, 2003, 18:22:55 Job time : 307.029 secs
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PCT-USO2-38216-18159
Sequence 18159, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: ROSetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/USO2/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 18159
LENGTH: 22
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; Sequence 25810, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILLE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 25810
; LENGTH: 19
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PCT-US02-38216-64492/c
; Sequence 64492, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: ROSECTEA GENOMICS LTD
; TITLE OF INVENTION: GENES AND USES THEREOF
; TITLE OF INVENTION: GENES AND USES THEREOF
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CORGANISM: Homo sapiens
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PCT-US02-38216-36515
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Pred. No. 4.2e+04;
0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: PCT/US02/38216
                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pr
Matches 13; Conservative 0;
                     CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.2
SEQ ID NO 64492
LENGTH: 19
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on:	October 27, 2003, 10:32:29 ; Search time 250.743 Seconds (without alignments) 1957.844 Million cell updates,	Search without 957.844	<pre>// Search time 250.743 Seconds (without alignments) 1957.844 Million cell updates/sec</pre>	Seconds updates/sec	
Title: Perfect score: Sequence:	US-09-331-204A-13 12 1 ggggtggtgggg 12	-	-		
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0			•	
Searched:	2888711 seqs, 20454813386 residues	sidues			
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18: em_hum:*

18: em_hum:*

22: em_ov:*

23: em_ph:*

24: em_hum:*

25: em_ph:*

26: em_hum:*

27: em_hum:*

28: em_htg_other:*

39: em_htg_other:*

31: em_htg_other:*

33: em_htg_other:*

34: em_htg_other:*

35: em_htg_other:*

36: em_htg_other:*

37: em_htg_other:*

38: em_htg_other:*

39: em_htg_other:*

40: em_htgo_mus:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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PAT 17-DEC-2001

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Unclassified.
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1 (bases 1 to 17)
Rando,R.F., Ojwaug,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
Rando,R.F., Ojwaug,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
Anti-viral guanosine-rich tetrad forming oligonucleotides
Anti-viral guanosine-rich tetrad forming oligonucleotides
Patent: US 6288042-A 64 11-SEP-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                          Unknown.
Unclassified.
1 (bases 1 to 17)
Rando,R.F., Ojwaug,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
Anti-viral guanosine-rich tetrad forming oligonucleotides
Anti-viral y 6288042-A 62 11-SEP-2001;
Patent: US 6288042-A 62 11-SEP-2001;
                                91.7%; Score 11; DB 6; Length 17; 100.0%; Pred. No. 2.5e+05; ive 0; Mismatches 0; Indels
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Sequence 65 from patent US 6288042.
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Sequence 62 from patent US 6288042.
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Sequence 64 from patent US 6288042.
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G-motif oligonucleotides and uses thereof
Patent: WO 0014217-A 42 16-MAR-2000;
LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ; WAGNER HERMANN (DE)
CPG IMMUNOPHARMACEUTICALS GMBH (DE)
Location/Qualifiers
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Viral hemorrhagic septicemia virus
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; Novirhabdovirus.
1 (bases 1 to 17)
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/organism="Viral hemorrhagic septicemia virus"
/mol_type="genomic DNA"
/db_xref="taxon:11287"
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100.0%; Score 12; DB 6; Length 18;
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Matches 12; Conservative 0; Mismatches 0; Indels
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="synthetic, no natural origin"
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Sequence 42 from Patent WO0014217.
AX023427
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A25058.1 GI:832954
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artificial sequences.
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RESULT 2 AX023427/c LOCUS

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PAT 20-APR-2002
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1 (bases 1 to 17)
Rando,R.F., Fennewald,S., Zendegui,J.G., Ojwang,J.O. and Hogan,M.E.
Anti-viral guanosine-rich oligonucleotides and method of treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT 29-JAN-2003
                                                                                                                                                                                                                                                                                      1 (bases 1 to 17)
Rando,R.F., Fennewald,S., Zendegui,J.G., Ojwang,J.O., Hogan,M.E.,
Pommier,Y. and Mazumder,A.
Guanosine-rich oligonucleotide integrase inhibitors
Patent: US 6355785-A 65 12-MAR-2002;
Location/Qualifiers
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Location/Qualifiers
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AR200308.
AR200308.1 GI:20250382
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Sequence 62 from patent US 6323185.
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AR262436.1 GI:28073867
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Unclassified.
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I Rando,R.F., Fennewald,S., Zendegui,J.G., Ojwang,J.O., Hogan,M.E., Pommier,Y. and Mazumder,A.
Guanosine-rich oligonucleotide integrase inhibitors
Patent: US 6355785-A 62 12-MAR-2002;
Location/Qualifiers
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Unclassified.
1 (bases 1 to 17)
Rando,R.F., Fennewald,S., Zendegui,J.G., Ojwang,J.O., Hogan,M.E.,
Pommier,Y. and Mazumder,A.
Guanosine-rich oligonucleotide integrase inhibitors
Patent: US 6355785-A 64 12-MAR-2002;
Location/Qualifiers
                                               Unknown.
Unclassified.
1 (bases 1 to 17)
Rando,R.F., Ojwaug,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
Anti-viral guanosine-rich tetrad forming oligonucleotides
Patent: US 6288042-A 65 11-SEP-2001;
Location/Qualifiers
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Pred. No. 2.5e+05;
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Sequence 64 from patent US 6355785.
AR200307.1 GI:20250381
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Sequence 62 from patent US 6355785.
AR200305
AR200305.1 GI:20250379
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Unclassified.

1 (bases 1 to 20)
Acton, S. Laurene.
Intronic and polymorphic SR-BI nucleic acids and uses therefor Patent: US 5998141-A 56 07-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l (bases 1 to 20)
Glazer, P.M.
Triple-helix forming oligonucleotides for targeted mutagenesis
Patent: US 5962426-A 2 05-OCT-1999;
Location/Qualifiers
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/organism="synthetic construct"
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kunstlichen
Sequenz:Polydesoxyribonukleotid"
) a 0 c 12 g 5 t
Patent: WO 0179487-A 36 25-OCT-2001;
Degitz, Klaus Karl (DE); Besch, Robert (DE)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 11; Conservative 0; Mismatches 0;
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Sequence 56 from patent US 5998141.
AR092032.
AR092032.1 GI:10018786
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Sequence 2 from patent US 5962426.
AR078333
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AR078333
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1 (bases 1 to 17)
Rando, R.F., Fennewald, S., Zendegui, J.G., Ojwang, J.O. and Hogan, M.E.
Anti-viral guanosine-rich oligonucleotides and method of treating
HIV
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1 (bases 1 to 17)
Rando,R.F., Fennewald,S., Zendegui,J.G., Ojwang,J.O. and Hogan,M.E.
Anti-viral guanosine-rich oligonucleotides and method of treating
HIV
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Location/Qualifiers
1..17
/organism="unknown"
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Location/Qualifiers
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              AR262438 17 bp
Sequence 64 from patent US 6323185.
AR262438
AR262438.1 GI:28073869
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Sequence 65 from patent US 6323185.
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AR262439.1 GI:28073870
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Sequence 36 from Patent WO0179487.
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AX284071.1 GI:17044781
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Search completed: October 27, 2003, 11:09:28 Job time : 251.743 secs

Triplex forming of CD28 inhibition of Human ETFB alleleOligonucleotide proligonucleotide SE Oligonucleotide HS ITANSCRIPTIONAL BE SEQUENCE OF B-133Sequence of B-133-

Run on:

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Reduction, T cell, CD28, gene expression, treatment, immune system, disorder, graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, interleukin 2, systemic lupus erythematosus, inflammatory bowel disease, IL-2, production, antisense, inhibition, ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD28 expression inhibiting oligonucleotide, RT18s.
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         AAZ99650
AAT36197
AAX90329
AAX90291
ABL39458
ABH83464
ABI20603
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ABF47470
ABF47471
ABH53376
ABH53377
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AAX79259

AAX79264

AAT68634

AAD096931

AAC81074

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95US-0529878.
95US-0387041.
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96WO-US01507
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16-APR-1997 (first entry)
WO9624380-A1
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18-SEP-1995;
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18-SEP-1995;
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(without alignments)
299.938 Million cell updates/sec
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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                   2552756 seqs, 1349719017 residues
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AAX90341
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The invention comprises DNA, cDNA and protein sequences of the human electron-transfer flavoprotein, beta polypeptide (ETFB) gene (located on chromosome 19q13.3-13.4). The invention specifically relates to the identification of 27 novel polymorphic sites within the ETFB gene.

Electron-transfer flavoprotein (ETF) is an obligatory electron acceptor of cr nine primary flavoprotein dehydrogenases and is located in the mitochondrial matrix. ETF is composed of an alpha (ETFA) and a beta mitochondrial respiratory chain by ETF dehydrogenases (ETFDA).

ETFB subunit. Electrons accepted by ETF are transferred to the mitochondrial respiratory chain by ETF dehydrogenases (ETFDA).

Deficiency of ETF or ETFDH leads to glutaric acidaemia type II (GAII).

Therefore ETFB is a pharmaceutically-important gene in the treatment of GAII. The novel ETFB polymorphisms identified in the invention are useful for studying the expression and function of ETFB in vivo. The ETFB protein and nucleic acids of the invention are useful for studying the acids are also useful for testing the efficacy of therapeutic agents and
AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated human electron-transfer-flavoprotein, beta polynucleotide, useful for therapeutic purposes, for studying the expression and function of the polynucleotide, and for expressing the flavoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             electron acceptor; mitochondrial matrix; glutaric acidaemia type II novel polymorphic site; novel polymorphism; ETFB genotype; ss; GAII ETFB haplotype; transgenic animal; primer; probe; chromosome 19q13; primer-extension oligonucleotide; single nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           electron-transfer flavoprotein beta polypeptide; ETFB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ETFB allele-specific oligonucleotide primer 19.
                                                                                                                                                                                  100.0%; Score 12; DB 20;
100.0%; Pred. No. 1e+04;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koshy
                                                                                                                                         Sequence 12 BP; 0 A; 0 C; 10 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kazemi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 14; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bieglecki KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВР.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2001; 2001WO-US21306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2000; 2000US-215984P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL39459 standard; DNA; 15
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                              present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200202580-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JAN-2002
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ABL39459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gabs
                                                                                                                                                                                                                                                                              The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ion, antisense oligonucleotide, interleukin 2; IL-2; mediated disease, gamma-interferon, IL-8;
                                                                                                                                     Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 12; DB 17; Length 1 illarity 100.0%; Pred. No. 1e+04; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD28 inhibiting phosphorothioate oligonucleotide RT18S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in cytokine release. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12 BP; 0 A; 0 C; 10 G; 2 T; 0 other;
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(ICNC ) ICN PHARM INC
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AAX90341 RESULT

Query Match

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Query Match
Best Local Similarity 100.
Matches 12, Conservative
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compounds for glutaric acidaemia type II. The nucleic acids of the invention are useful in the production of a transgenic animal expressing the ETFB gene. Nucleic acids ABL39414-ABL39440 represent claimed ETFB allele-specific probes. Nucleic acids ABL39441-ABL39494 represent claimed ETFB allele-specific PCR primers. Nucleic acids ABL39495-ABL39548 represent claimed ETFB primer-extension pligonucleotides.
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                            Reduction, T cell, CD28, gene expression, treatment, immune system, disorder; graft versus host disease; septic shock, viral disease, psoriasis, type I diabetes mellitus; thyroiditis; sarcoides, multiple sclerosis, uveitis; rheumatoid arthritis, 5'-UTR, systemic lupus erythematosus; inflammatory bowel disease; triplex forming; oligonucleotide; 5'-untranslated region; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present oligonucleotide reduces T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.

(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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                                                                                                           Match 100.0%; Score 12; DB 24; Length 15; Local Similarity 100.0%; Pred. No. 1e+04; les 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                      Triplex forming oligo targetting CD28 5'-UTR (nt 58-75).
                                                                                     Sequence 15 BP; 0 A; 0 C; 11 G; 3 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 1 A; 0 C; 13 G; 4 T; 0 other,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0387041.
95US-0529878.
95US-0387041.
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(first entry)
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18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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15-APR-1997
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                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD28 inhibiting phosphorothioate oligonucleotide RT03S
100.0%; Score 12; DB 17;
100.0%; Pred. No. 9.9e+03;
ive 0; Mismatches 0;
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AAX90332/c
ID AAX90332 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                  AAX90328 standard; DNA; 18
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The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated
                                                                                                                                               The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. AAX90292 to AAX90323 represent oligonucleotides used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD28, inhibition, antisense oligonucleotide, interleukin 2, IL-2, immune system mediated disease, gamma-interferon, IL-8, ss.
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                                                    Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
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100.0%; Pred. No. 9.9e+03;
cive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 9.9e+03; Matches 12; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                     Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Column 29; 45pp; English
                                                                                                              Example; Column 13; 45pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-443609/37.
               WPI; 1999-443609/37.
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 12, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothioate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; ss.
                                    CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; phosphorothicate; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 12; DB 20; Length 1 Best Local Similarity 100.0%; Pred. No. 9.9e+03; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide RTC06 used in an Example from US5932556.
CD28 inhibiting phosphorothicate oligonucleotide RTC06S.
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ID AAX90297 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-443609/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention
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                                                                                                                 Synthetic.
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Best Loc Matches

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Gaps

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Tam RC

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17

7 GGGGTGGTGGGG 18

AAZ99625 standard; DNA; 18 BP AAZ9962

12-JUL-2000 (first entry) AAZ99625;

Nucleotide seguence of G-motif oligonucleotide GR1.

G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection; antigen presenting cell activation; natural killer cell; septic shock; cytotoxic T-lymphocyte; inflammation; autoimmune disease; rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis; Kawasaki syndrome; graft-versus-host disease; transplant rejection; helper T cell response 1-mediated disease; Lyme arthritis; streptococcal induced arthritis; chronic inflammatory bowel disease; psoriasis vulgaris; experimental allergic encephalomyelitis; insulin-dependent diabetes mellitus; bacterial infection; parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss

Synthetic

WO200014217-A2.

16-MAR-2000

99WO-EP06502 03-SEP-1999;

03-SEP-1998;

(CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

Heeg K; Wagner H, Lipford GB,

WPI; 2000-256970/22.

Compositions comprising G-motif oligonucleotides useful for treating e.g. septic shock, rheumatoid arthritis, diabetes and human immunodeficiency virus infections -

Example 14; Page 32; 75pp; English

The present sequence represents a G-motif oligonuclectide of the invention. The specification describes compositions comprising G-motif oligonucleotides inhibit activation of antigen presenting cells by inhibiting the uptake of DNA by a cell, by stimulating natural killer cells, or by co-stimulating cytotoxic T-lymphocytes. The G-motif oligonucleotides may be used for the productions of vaccines for treating septic shock, inflammation, autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease, carcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host disease and transplant rejection), helper T cell response 1-mediated diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic inflammatory bowel disease, psoriasis vulgaris, experimental allergic encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis), viral infections (e.g. Cytomegalovirus and human immunodeficiency virus (HIV)-infections), spontaneous abortions and tumours. They may also be used to induce proliferation of bone marrow cells, especially macrophage

The present sequence represents a non-G-motif oligonucleotide of the invention. The specification describes compositions comprising G-motif oligonucleotides inhibit activation of antigen presenting cells by inhibiting the uptake of DNA by a cell, by stimulating natural killer cells, or by co-stimulating cytotoxic continulating natural killer cells, or by co-stimulating cytotoxic continulating natural killer cells, or by co-stimulating cytotoxic continulating natural killer cells, or by co-stimulating cytotoxic continulations of vaccines for treating septic shock, inflammation, autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease, cautoimmune disease, continulating careforms, inflammatory bowel disease, psoriasis vulgaris, byme arthritis, chronic inflammatory bowel disease, psoriasis vulgaris, experimental allergic encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis), continulation (e.g. Cytomegalovirus and human immunodeficiency virus infections).

Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;

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Gaps
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Similarity
Query Match
Best Local Simi
Matches 12;
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Gaps

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100.0%; Score 12; DB 21; Length 18; larity 100.0%; Pred. No. 9.9e+03; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 12; Conserv

Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;

cells, especially macrophage

ifections), spontaneous abortions and tumours. They induce proliferation of bone marrow cells, especial

(HIV) -infections),

used to

human immunodeficiency virus of tumours. They may also be

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G-motif oligonuclectide, vaccine, Toxoplasmosis, viral infection, antigen presenting cell activation, natural killer cell, septic shock, cytotoxic T-lymphocyte, inflammation, autoimmune disease, rheumatoid arthritis, Crohn's disease, sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host disease, transplant rejection, helper T cell response 1-mediated disease, Lyme arthritis, streptococcal induced arthritis, chronic inflammatory bowel disease, psoriasis vulgaris, experimental allergic encephalomyelitis, insulin-dependent diabetes mellitus; bacterial infection, tumour, ss. parasitic infection, Leishmaniasis, spontaneous abortion, tumour, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Compositions comprising G-motif oligonucleotides useful for treating e.g. septic shock, rheumatoid arthritis, diabetes and human immunodeficiency virus infections -
                                                                                                                                                          Nucleotide sequence of non-G-motif oligonucleotide GRF1comp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
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                                                                                 AAZ99650 standard; DNA; 18
                                                                                                                                    (first entry)
1 GGGGTGGTGGGG 12
                     decendences 18
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                                                                                                                                                                                                                                                                                                                                                 WO200014217-A2.
                                                                                                                                                                                                                                                                                                                                                                                                   03-SEP-1999;
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                                                                                                                                    12-JUL-2000
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                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                           AAZ99650;
                                                                      AAZ99650,
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2; IL-2;

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The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN).

AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
                                                                                                                                    CD28; inhibition; antisense oligonucleotide; interleukin
immune system mediated disease; gamma-interferon; IL-8;
                                                                                                     CD28 inhibiting phosphorothioate oligonucleotide RT04S.
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100.0%; Pred. No. 9.8e+03;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD28 inhibition oligonucleotide RT04.
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ВР
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Best Local Similarity 100...
Thes 12; Conservative
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AAX90329 standard; DNA; 21
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                                                                     (first entry)
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                                                                                                                                                                             phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-443609/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention.
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                                                                      24-SEP-1999
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                                                                                                                                                                                                               Synthetic.
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                                 AAX90329;
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AAX90291
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                                                                                                                                                                                                                                                                                                Reduction; T cell; CD28; gene expression; treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; psoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR; systemic lupus erythematosus; inflammatory bowel disease; triplex forming; oligonucleotide; 5'-untranslated region; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present oligonuclectide reduces T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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                                                                                                                                                                                                                                                               Triplex forming oligo targetting CD28 5'-UTR (nt 58-78).
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                                                                                                                                          BP.
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95US-0529878.
95US-0387041.
95US-0529878.
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                                                                                                                                       AAT36197 standard; DNA; 21
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(first entry)
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Best Local Similarity 100.
Matches 12; Conservative
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18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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15-APR-1997
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Tam RC;

Synthetic

AAT36197;

RESULT 11 AAT3619

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Gaps

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Indels

95US-0529878.

18-SEP-1995;

RESULT 12 AAX90329

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Length 21;

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chromosome 19q13.3-13.4). The invention specifically relates to the chromosome 19q13.3-13.4). The invention specifically relates to the identification of 27 novel polymorphic sites within the ETFB gene.

C Electron-transfer flavoprotein (ETF) is an obligatory electron acceptor of or alpha (ETFA) and a beta controlly subunit. Electrons accepted by ETF are transferred to the mitochondrial respiratory chain by ETF dehydrogenases (ETFDHs).

CC All The novel ETFB polymorphisms identified in the invention are useful for testing the efficacy of therapeutic agents and compounds for glutaric acides ABL39414 and septembered to compounds for glutaric acides ABL39414 ABL39441 represent claimed ETFB allele-specific probes. Nucleic acide ABL39414-ABL39494 represent claimed ETFB primer-extension oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous; system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 283457 for detecting SNP TSC0011318.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Set of oligonuclectides, useful for diagnosis and cell designed to detect single nucleotide polymorphisms and methylation status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 11.6; DB 24;
Pred. No. 1.5e+04;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15 BP; 3 A; 10 C; 1 G; 0 U; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.7%;
91.7%;
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ABH83464 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-657177/75.
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                                                                                                                                                                                                                                                                                                         The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention comprises DNA, cDNA and protein sequences of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated human electron-transfer-flavoprotein, beta polynucleotide, useful for therapeutic purposes, for studying the expression and function of the polynucleotide, and for expressing
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                                                                                                                                                                                                 system-mediated diseases by inhibiting IL-2, gamma-interferon or IL-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ETFB allele-specific oligonucleotide primer 18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 12; DB 20; 100.0%; Pred. No. 9.8e+03;
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                                                                                                                                                                                                                                                                  Claim 6; Column 29; 45pp; English
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                              95US-0529878
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                              18-SEP-1995;
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CC range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and CC ABC00010-ABI82073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed CC Specification, but was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 12 BP; 2 A; 10 C; 0 G; 0 U; 0 other;
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 Query Match
 91.7%; Score 11; DB 23; Length 12;

 Best Local Similarity 100.0%; Pred. No. 2.9e+04;

 Matches 11; Conservative 0; Mismatches 0; Indels

 Qy
 1 GGGGTGGTGGTGG 11

 Db
 11 GGGTGGTGGTGG 1

.. 0

Gaps

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Search completed: October 27, 2003, 11:25:21 Job time : 108 secs

0.4 86.7 19 28 AZ447936 AZ447936 IM024 0.4 86.7 19 28 AZ780591 AZ780591 AZ786308 ZM003 0.4 86.7 20 28 AZ786338 AZ786338 AZ7865238 IM027	86.7 21 28 AZ495585 1M0331H0 86.7 21 28 AZ774703 2M0004G1 86.7 22 9 AI183338 AI183338 Qd41a12.x 86.7 22 9 AI439277 Li54a02.x 86.7 22 28 AZ766712 AZ766712 1M0564A0 86.7 22 28 AZ769521 AZ769521 1M057001	10 83.3 19 9 AA928040 AA928040 oi58gG 10 83.3 21 28 A2758704 AZ758704 IMO55 10 83.3 22 9 AA923820 AA923820 O190bG 10 83.3 22 9 AI354432 AI354432 QU17dG .4 78.3 16 9 AI569544 AIS69544 CO28d1	78.3 16 9 AI684114 AI684114 tx79d02.x 78.3 19 9 AA909236 AA909236 ol08a11.s 78.3 19 9 AI364573 AI364573 Qw37g03.x 78.3 21 28 AZ468862 AZ468862 1M028200 78.3 21 28 AZ512534 AZ512534 1M0358B0	.4 78.3 21 28 AZ783943 AZ783943 2M002 .4 78.3 21 28 AZ788597 AZ788597 2M003 .4 78.3 21 28 AZ864022 AZ864022 AZ864022 2M017 .4 78.3 22 9 AI687266 TP94d1	.4 78.3 22 9 AI707945 AI707945 as34910.x .4 78.3 22 13 BQ585098 BQ585098 B0118264 78.3 22 28 AZ327083 AZ327083 IM0050D1 .4 78.3 22 28 AZ454940 AZ454940 IM0257B1	.4 78.3 22 28 A252793 .4 78.3 22 28 A295302 9 75.0 21 28 A239982 .8 73.3 12 13 BQ59501 .8 73.3 14 13 BQ59501 .8 73.3 16 9 AA937364 .8 73.3 16 9 AA956729	.8 73.3 16 9 AI209036 AI209036 GG18G18G18G18G18G18G18G18G18G18G1	AIS90540 LWILC02.xl NCI CGAP Brn52 Homo sapiens CDNA	AIS90540. AIS90540.1 GI:4599588 EST. Homo sapiens (human) M Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrat Mammalia; Eutheria; Primates; Catarrhini; Hominid	1 (bases 1 to 16) NCI/NINDS-CGAP http National Cancer Ins Disorders and Stroy (CGAP/BTGAP), Tumou	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
			00000			O O D O D O D O O O O O O O O O O O O O		RESULT 1 A1590540/c LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE ORGANISI	REFERENCE AUTHORS TITLE JOHNAL	COMMENT
5.1.6 Compugen Ltd.	earch time 1054.51 Seconds .hout alignments) 576 Million cell updates/sec		dues	rs: 11152						cted by chance to have a of the result being printed, score distribution.	Description AIS90540 tw11002.x AI807936 wf52e09.x AZ369361 1M0119123 AZ381799 1M0138G01
GenCore version 5. Copyright (c) 1993 - 2003 Co	OM nucleic - nucleic search, using sw model Run on: October 27, 2003, 10:32:29; Se (wit	US-09-331 Score: 12 e: 1 9999t99	ng table: IDENTITY NUC Gapop 10.0 , Gap hed: 22781392 seqs, 1	Total number of hits satisfying chosen paramete Minimum DB seq length: 0 Maximum DB seq length: 22	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database: 1: em_estba:* 2: em_esthum:* 3: em_estin:* 4: em_estin:* 5: em_estin:* 7: em_estpl:* 7: em_estro:*			2: em_gas_mam: 4: em_gas_mam: 5: em_gas_pro: 6: em_gas_pro: 6: em_gas_pro: 7: em_gas_pro: 7: em_gas_vrl: 8: gb_gas1:*	<pre>9: gb_gss2:* s the number of results predi er than or equal to the score ved by analysis of the total</pre>	Result Query No. Score Match Length DB ID C 1 10.4 86.7 16 9 A1590540 C 2 10.4 86.7 19 28 AZ369361 4 10.4 86.7 19 28 AZ369361

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AZ369361
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                                                                                                                                                                   1. 16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2259362"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH108"
/clone_lib="NCI_GGAP_Brn52"
/lab_host="DH108"
/clone_lib="NCI_GGAP_Brn52"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; This library represents the normalized
version of NCI_GGAP_Brn35. Cloned unidirectionally.
Primer: Oligo_dT. Average insert size 1.19 kb. Tumor
types include: meningioma, oligodendroglioma, astrocytoma
(grade II), medulloblastoma, astrocytoma (grade IV).
Constructed by Life Technologies."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2359240"
/lab_host="DH10B"
/clone_lib="Soares NFL_T_GBC_S1"
/note="Organ: pooled, Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker, Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNĀ from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 19)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished
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W£52e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2359240 3' similar to TR:Q39600 Q39600 EXTENSIN. ;contains
element_MSR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 724 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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www-bio.llnl.gov/bbrp/image/image.html
                                    Trace considered overall poor quality Insert Length: 353 Std Error: 0.00 Seq primer: -400P from Gibco High quality sequence stop: 1 POLYA=No.
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Homo sapiens
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INOI19123R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0119123 R, genomic survey sequence.
AZ369361.
AZ369361.1 GI:10483061
NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Patima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 19)

Dunn,D., Acyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,R., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.ed"
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Pred. No. 6.9e+05;
0; Mismatches 1;
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Insert Length: 10000 Std Error: 0.00
Plate: 0119 row: I column: 23
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0119123"
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Seg primer: CACACAGGAAACAGCTATGACC
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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l Similarity 91.7%;
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11; Conservative
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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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19 bp DNA linear GSS 02-OCT-200

1M0138G01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0138G01 R, genomic survey sequence,
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/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0138 row: G column: 01
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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strain="C57BL/6J"
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clone="UUGC1M0138G01"
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AZ381798.1 GI:10495498
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ilarity 91.7%;
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TITLE

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FEATURES

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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0245 row: O column: 18
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0245018"
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Location/Qualifiers
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ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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AZ780591.1 GI:12912422
GSS.
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

I (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
"m 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0018 row: B column: 09
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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Location/Qualifiers
1. 19
/organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="tuGC2M0018B09"
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Matches 11; Conserv
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AZ786308
AZ786308.1 GI:12923936
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 19)
Dunn,D., Acyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
Mouse whole genome scaffolding with paired end reads from 10kb
Unpublished
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/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Pred. No. 6.9e+05;
0; Mismatches 1; Indels C
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
84112, USA
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Insert Length: 10000 Std Error: 0.00
Plate: 0031 row: B column: 17
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/organism="Mus musculus"
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91.7%;
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Fax: 801 585 7177
Email: ddunn@genet
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polynuclectide kinase. Maptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished
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was blunt end-repaired with T4 DNA polymerase and T4
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Pred. No. 6.9e+05;
0; Mismatches 1; Indels (
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0276 row: J column: 16
Seg primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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/clone="UUGC1M0276J16"
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11; Conservative
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Fax: 801 585 7177
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was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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AZ495585
AZ495585.1 GI:10671122
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PwD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A.

Mouse whole genome scaffolding with paired end reads from 10kb
Unpublished
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Pred. No. 6.9e+05;
0; Mismatches 1;
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91.7%;
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Mus musculus (house mouse)

Mus musculus (house mouse)

Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;

Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

I (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, example of the into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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AZ774703
AZ774703.1 GI:12900261
GSS.
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from Musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0004 row: G column: 14
Seg primer: CGTTGTAAAACGACGACGT
Class: plasmid ends
High quality sequence stop: 21.
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/organism="Mus musculus"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified molareses gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptores complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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NCI - CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished
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Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality
Insert Length: 698 Std Error: 0.00
Seg primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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/mol_type="mRNA"
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/clone="IMAGE:1732030"
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Ali83338.1 GI:3733976
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Homo sapiens
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1M0564A03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0564A03 R, genomic survey sequence. AZ766712
                                                                                                                                                      Mus musculus (house mouse)
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/clone lib="NCI_CGAP_Lyml2"
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Sall; Site_2: Not1; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"

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/organism="Homo sapiens"
/organism="Homo sapiens"
/dol_type="mxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:2134250"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 22)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
     M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."
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0; Mismatches 1; Indels
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Pred. No. 7e+05;
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Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Homo sapiens
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/ organism="Mus musculus"
/mol_type="genomic DNA"
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/db_xref="Texacon:10090"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone="UuGCIMO564A03"
/sex="Muscoli DNA Purified genomic DNA from M.
was hydrodynamically seources/documents/dnares/). The DNA
was hydrodynamically seources/documents/dnares/). The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuleocide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli xL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                          Unpublished Contact: Robert B. Weiss University of Utah Genome Center University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 84112, USA 112, USA 112, USA 112, USA 113, USA 114, USA 115, USA 115, USA 115, USA 115, USA 116, USA 117, USA 11801 S85 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0564 row: A column: 03 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
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Location/Qualifiers
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Email: cgapbs-remail.nih.gov
Tissue Procurement: John Ensley, M.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                         AA928040 19 bp mRNA linear EST 22-APR-1998 oi58g09.s1 NCI CGAP HN4 Homo sapiens cDNA clone IMAGE:1486912 3' similar to TR:\(\overline{004216}\) 004216 EXTENSIN ; contains element MSR1 repetitive element ;, mRNA sequence.
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1 (bases 1 to 19)
NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Dental Research, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                AA928040
AA928040.1 GI:3077196
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P
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AZ769521
1M0570018F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0570018 F, genomic survey sequence.
                                                                                                                                               Mus musculus (house mouse)
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R.,

Muright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0570 row: O column: 18
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/60"
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/clone="UUGC1M0570018"
                                                                                                     AZ769521.1 GI:12889741
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91.78;
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11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                              AZ769521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local 9
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ORIGIN
                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
      LOCUS
DEFINITION
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                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                    TITLE
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/ Organish = now Sapiens
/ And type="mRNA"
/ db xref="taxon:9606"
/clone="IMAGE:1486912"
/tissue_type="squamous cell carcinoma"
/tissue_type="squamycin resistant)"
/clone lib="NCI CGAP HN4"
/note="Gorgan: pharynx; Vector: Bluescript SK-; Site_1:
EcoRI, Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.5 kb. 5' adaptor sequence:
5' GAATTCGGCACGAG 3' 3' adaptor sequence: 5' (GA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
O
                                                                                                                                                                                                                                                                                                                                                                                                             83.3%; Score 10; DB 9; Length 19;
100.0%; Pred. No. 1e+06;
iive 0; Mismatches 0; Indels
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ne : 1055.51 secs
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ò a Sequence

Sequence 2, Appli Sequence 13, Appl Sequence 13, Appl Sequence 31, Appl Sequence 63, Appl Sequence 20, Appl Sequence 21, Appl Sequence 22, Appl Sequence 174, Appl Sequence 10, Appl

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Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
US-08-529-878B-3
; Sequence 3, Application US/08529878B
; Patent No. 5932556
; GENERAL INFORMATION:
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
; VUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Crockett & Fish
; STREET: 3000 S. Augusta Court
; CITY: La Habra
; STATE: California
; COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 12; DB 2; L
.larity 100.0%; Pred. No. 1.1e+03;
Conservative 0; Mismatches 0;
US-09-429-130-11
US-08-580-242-2
PCT-US94-0631A-22
US-08-469-802B-13
US-09-469-802B-13
US-09-513-729B-63
US-09-662-249A-21
US-09-662-249A-10
US-08-987-574-10
US-08-98-535-168-10
US-08-987-574-10
US-08-682-255A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fish, Robert D.
REGISTRATION NUMBER: 213/003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 714-525-3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic)
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SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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       nucleic acid
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nuclei
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-529-878B-3
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                                                                                                                                                   October 27, 2003, 10:32:34; Search time 27.5429 Seconds (without alignments) 192.304 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 45, Sequence 62, Sequence 64, Sequence 65, Sequence 65, Sequence 65, Sequence 65, Sequence 64, Sequence 64, Sequence 64, Sequence 64, Sequence 64, Sequence 65, Sequence 64, Sequence 65, Seque
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Sequence 44,
Sequence 48,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2
Sequence 3
Sequence 3
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lssued_Patents NA:*

'cgn2_6/ptodata/1/ina/5A_COMB.seq:*
'cgn2_6/ptodata/1/ina/5B_COMB.seq:*
'cgn2_6/ptodata/1/ina/6A_COMB.seq:*
'cgn2_6/ptodata/1/ina/6B_COMB.seq:*
'cgn2_6/ptodata/1/ina/6B_COMB.seq:*
'cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
'cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-529-878B-3
US-08-529-878B-44
US-08-529-878B-44
US-08-529-878B-44
US-08-529-878B-4
US-08-529-878B-4
US-09-017-974-64
US-09-017-974-64
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US-09-429-130-65
US-09-031-656
US-09-031-626-56
US-08-387-774-11
US-08-37-71-11
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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12
1 ggggtggtgggg 12
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Match Length DB
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Maximum DB seq length: 22
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Perfect score:
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                                                                                                                                                                                                                                                                                                     Sequence:
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Gaps

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US-08-529-878B-48/C

Sequence 48, Application US/08529878B

Patent No. 5932556

GENERAL INFORMATION:

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS: 48

CORRESPONDENCE ADDRESS: 48

CONTRY: La Habra

STATE: 2010 S. Augusta Court

CITY: La Habra

COUNTRY: United States of America

STATE: 1000 S. Augusta Court

CITY: La Habra

COUNTRY: United States of America

STATE: PO031

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: BM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6:1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/529,878B

FILING DATE: 13-SEP-1995

CLASSIFICATION NUMBER: 213/003

TELECOMMUICATION INPORMATION:

REFERENCE/DOCKET NUMBER: 213/003

TELEPHONE: 714-525-3303

TELEFHONE: 714-525-3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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                        UMBER: US/08/529,878B
13-SEP-1995
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,
FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fish, Robert D.
REGISTRATION NUMBER: 33,880
REFERENCE/DOCKET NUMBER: 213/C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-525-3433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-529-878B-44
                                                                                                                                                                                                                                                                                                                                                TELEX:
INFORMATION FOR SEQ ID NO: 4'
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGGTGGTGGGG 12
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                                                          WESTOLITY

US-08-529-878B-10/C

IS-08-529-878B-10/C

Sequence 10, Application US/08529878B

Patent No. 5932556

GENERAL INFORMATION:

APPLICANT: Tam, Robert C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: Crockett & Fish STREET: 3000 S. Augusta Court CITY: La Habra STREET: 3000 STREET: 3000 STREET: 3000 STREET: 3000 STREET: 33,880

REFERENCE/DOCKET NUMBER: 213/003

TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

Sequence 44, Application US/08529878B

Patent No. 5932556

GENERAL INFORMATION:

APPLICANT: Tam, Robert C.

TITLE OF INVENTION: RETHODS AND COMPOSITIONS FOR

TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSE: Crockett & Fish

STREET: 3000 S. Augusta Court

CITY: La Habra

STATE: California

COUNTRY: United States of America

ZIP: 90631

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: WordPerfect 6.1

SOFTWARE: WordPerfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; STRANDEDNESS: unknown; TOPOLOGY: unknown; MOLECULE TYPE: DNA (genomic) US-08-529-878B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 714-525-343
TELEFAX: 714-525-3303
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGGTGGTGGGG 12
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Sequence 62, Application US/09017974

GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
APPLICANT: Ojwang, Joshua O.
APPLICANT: Hogan, Michael E.
APPLICANT: Wallace, Thomas L.
APPLICANT: Cossum, Paul A.
ITLE OF INVENTION: Anti-Viral Guanosine-Rich
ITLE OF INVENTION: Anti-Viral Guanosine-Rich
ITLE OF INVENTION: Anti-Viral Guanosine-Rich
CORRESPONDENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
STREET: 600 Travis, Suite 1800

CITY: Houston
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ZIP: 77002-2912
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word 97 (saved as .txt file)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,974
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 60/037,374
FILING DATE: 09-DEC-97
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
COUNTRY: United States of America ZIP: 90631
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/529,878B FILING DATE: 13-SEP-1995 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION: NAME: Fish, Robert D. REGISTRATION NUMBER: 33,880
REFERENCE/DOCKET NUMBER: 213/003
TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECHONE: 714-525-3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-529-878B-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 12; Conservative
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                                          0; Gaps
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            Pred. No. 1.1e+03;
; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                    US-08-529-878B-4

| Sequence 4, Application US/08529878B
| Patent No. 5932556
| GENERAL INFORMATION:
| TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION UNBER OF SEQUENCES: 48
| CORRESPONDENCE ADDRESS:
| ADDRESSE: Crockett & Fish CONTESTONED OF COURT CITY: La Habra STATE: California COUNTEY: United States of America CITY: La Habra STATE: California COUNTEY: United States of America CONFUTER: WordPerfect 6.1
| COMPUTER: WordPerfect 6.1
| COMPUTER: WordPerfect 6.1
| CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/529,878B
| FILING DATE: 13.56P-1995 CLASSIFICATION NUMBER: 213/003 TELECOMMUNICATION INFORMATION: NEGLERBANCE/DOCKET NUMBER: 213/003 TELECOMMUNICATION INFORMATION: TELECOMUNICATION INFORMATION: TELECOMMUNICATION
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Patent No. 5932556
GENERAL INFORMATION:
APPLICANT: Tam, Robert C.
APPLICANT: Tam, Robert C.
TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Crockett & Fish
STREET: 3000 S. Augusta Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 1
Matches 12; Conservative 0; Mismatche
          Best Local Similarity 100.0%; P
Matches 12; Conservative 0;
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; MOLECULE TYPE: DNA (genomic)
US-08-529-878B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX:
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGGGTGGTGGGG 12
                                                                                                  1 GGGGTGGTGGGG 12
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                                                                                                                                                          18 ĠĠĠĠĠĠĠĠĠĠĠĠ 7
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US-08-529-878B-45
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US-09-017-974-65

US-09-017-974-65

Sequence 65, Application US/09017974

Patent No. 638842

GENERALINGMEATION:
APPLICANT: Oyang, Joshua O.
APPLICANT: Oyang, Joshua O.
APPLICANT: Wallace, Thomas L.
APPLICANT: Wallace, Thomas L.
APPLICANT: Cossum, Paul Ant. viral Guanosine-Rich
TITLE OF INVENTION: Tetrad Forming Oligonuclectides
UNTHER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
STATE: Houston
STATE: Pacas
COMPUTER READABLE FORM:
MEDIOM TYPE: PLOPPY disk
COMPUTER READABLE FORM:
MEDIOM TYPE: PLOPPY disk
COMPUTER READABLE FORM:
MEDIOM TYPE: PLOPPY disk
COMPUTER: US-A.

ZIP: 7700-2912

COMPUTER: US-A.
ZIP: 7700-2912

COMPUTER: US-A.

SOFTWARE: PO-POS/MS-DOS
SOFTWARE: WS WORD G) 7 (saved as .txt file)
FILING DATE: O9-DEC-97

PILING DATE: O9-DEC-97

APPLICATION NUMBER: US/09/017,974

FILING DATE: WS-READABLE COMPUTER: US-DEC-97

APPLICATION NUMBER: US-DEC-97

APPLICATION NUMBER: US-DEC-97

APPLICATION NUMBER: 1472-06223

TELEBHONE: T13/238-8010

TELEBHONE: 713/238-8010
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        Length 17;
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100.0%; Pred. No. 3.3e+03;
tive 0; Mismatches 0;
     91.7%; Score 11; DB 3; Lv
100.0%; Pred. No. 3.3e+03;
iive 0; Mismatches 0;
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LOCATION: 5

CTHER INFORMATION: /note= "C-5 propynl dU"

US-09-017-974-65
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
           Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
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Matches 11; Conserv
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Sequence 64, Application US/09017974

Patent No. 6288042

GENERAL INFORMATION:

APPLICANT: Rando, Robert F.

APPLICANT: Hogan, Michael E.

APPLICANT: Hogan, Michael E.

APPLICANT: Gossum, Michael E.

APPLICANT: Cossum, Michael E.

APPLICANT: Cossum, Michael E.

APPLICANT: Adlace, Thomas L.

APPLICANT: Cossum, Michael E.

STREET: Conservation, Anti-Viral Guanosine-Rich

CORRESPONDENCE ADDRESS:

ADDRESSEE: Conley, Rose & Tayon, P.C.

STREET: GOO Travis, Suite 1800

CITY: Houston

STREET: Conput, Rose & Tayon, P.C.

STREET: GOO Travis, Suite 1800

CITY: Houston

STREET: Fexas

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: MS WOAG 97 (saved as .txt file)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/017,974

FILING DATE:

FILING 
REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06223
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/238-8010
TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-017-974-62
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,374
FILING DATE: 04-FEB-97
APPLICATION NUMBER:
FILING DATE: 09-DEC-97
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06223
TELEPHONE: 713/238-8010
TELEPHONE: 713/238-8010
TELEPHONE: 713/238-8010
TELEFAX: 713/238-8010
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Best Local Similarity 100.
Matches 11, Conservative
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RESULT 10

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                                                        APPLICANT: Sendegui, Joseph G.
APPLICANT: Downer, Joshua O.
APPLICANT: Hogan, Michael E.
APPLICANT: Hogan, Michael E.
APPLICANT: Hogan, Michael E.
APPLICANT: Pommier, Eyves
APPLICANT: Maxumder, Abhilit
TITLE OF INVENTION: Oligonuclectides
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
CITY: House Conjection of C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.3e+03
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APPLICANT: Rando, Robert F.
APPLICANT: Fennewald, Susan
APPLICANT: Zendegui, Joseph G.
APPLICANT: Ojwang, Joshua O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.7%; SCC-
100.0%; Pre
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Best Local Similarity 100.
Matches 11; Conservative
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US-08-682-255A-65
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                 GENERAL INFORMATION:

APPLICANT: Rando, Robert F.

APPLICANT: Fennewald, Susan

APPLICANT: Zendegui, Joseph G.

APPLICANT: Ojwang, Joshua O.

APPLICANT: Pomier, Eyves

APPLICANT: Mazumder, Abhijit

TITLE OF INVENTION: Oligonucleotides

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:

ADDRESSEE: Conley, Rose & Tayon, P.C.

STREET: 600 Travis, Suire 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Texas

COUNTY: 10.S.A.

ZIP: 77002-2912

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: MS Windows 95

SOFTWARE: MS Word 97 (saved as .txt file)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/682,255A

FILING DATE: 17-JULY-1996

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: 60/01,505

FILING DATE: 23-OCT-95

APPLICATION NUMBER: 60/014,007

FILING DATE: 19-JULY-95

APPLICATION NUMBER: 60/013,688

FILING DATE: 19-MARCH-96

APPLICATION NUMBER: 60/015,714

FILING DATE: 17-APRIL-96

APPLICATION NUMBER: 60/016,271

FILING DATE: 17-APRIL-96

APPLICATION NUMBER: 60/016,271

FILING DATE: 17-APRIL-96

APPLICATION NUMBER: 60/016,271

FILING DATE: 17-APRIL-96

APPLICATION NUMBER: 33,962

REFERENCE/DOCKET NUMBER: 1472-06214

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 64, Application US/08682255A Patent No. 6323185 GENERAL INFORMATION:
                         Sequence 62, Application US/08682255A
Patent No. 6323185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 11; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linea
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US-08-682-255A-64
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US-08-682-255A-62
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Length 17;
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SOUNTRY: U.S.A.

ZIP: 77002-2912

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS Windows 95

SOFTWARE: MS Word 97 (saved as .txt file)
  Hogan, Michael E.
Pommier, Eyves
Mazumder, Abhijit
60/015,714
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
Oligonucleotides
NUMBER OF SEQUENCES: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.3e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: *UNKNOWN PELLING DATE: *UNKNOWN PELLING DATE: 19-JULY-95

FILING DATE: 19-JULY-95

APPLICATION NUMBER: 60/014,007

FILING DATE: 25-MARCH-96

APPLICATION NUMBER: 60/013,688

FILING DATE: 19-MARCH-96

APPLICATION NUMBER: 60/016,271

FILING DATE: 17-APRIL-96

ATTORNEY/AGENT INFORMATION:

NAME: McDaniel, C. Steven

REGISTRATION NUMBER: 33,962

REFERENCE/DOCKET NUMBER: 1472-06214

TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.7%; Score 11; DB 4;
100.0%; Pred. No. 3.3e+0
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/429,130
FILING DATE: 28-Oct-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                           NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon,
STREET: 600 Travis, Suite 1850
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 62:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/682,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APRIL-96
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Patent No. 6355785
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
Fennewald, Susan
Zendegui, Joseph G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 713/238-8010
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INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             near
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Best Local Similarity 100.
Marches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGGTGGTGGG 11
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US-09-429-130-64
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                                                                                                                                                                                                                                                                   CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77002-2912
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: MS WORD 97 (saved as .txt file)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,255A
FILING DATE: 17-JULY-1996
CLASSIFICATION NUMBER: 60/001,505
FILING DATE: 19-JULY-95
APPLICATION NUMBER: 60/014,007
FILING DATE: 19-JULY-95
APPLICATION NUMBER: 60/013,688
FILING DATE: 19-JULY-96
APPLICATION NUMBER: 60/015,714
FILING DATE: 17-APRIL-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 17-APRIL-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 17-APRIL-96
APPLICATION NUMBER: 1472-06214
TELECOMMUNICATION INFORMATION:
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THE TELECOMMUNICATION INFORMATION:
THE TELECOMMUNICATION INFORMATION:
APPLICANT: Hogan, Michael E.
APPLICANT: Pommier, Eyves
APPLICANT: Mazumder, Abhijit
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
STREET: 600 Travis, Suite 1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature;

LOCATION: 5

CTHER INFORMATION: /note= "C-5 propynl dU"

US-08-682-255A-65
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US-09-429-130-62
; Sequence 62, Application US/09429130
; Patent No. 6355785
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; Fennewald, Susan
; Zendegui, Joseph G.
; Ojwang, Joshua O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOLECULE TYPE: DNA (genomic) PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGGGTGGTGGG 11
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Best Local Similarity
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Gaps
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                                                                                                                                                                                                                                                                    CITY: Houston
STATE: Houston
STATE: Houston
STATE: Tows
COUNTRY: U.S.A.
ZIP: 77002-2912
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: MS Word 97 (saved as .txt file)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/429,130
FILING DATE: 28-Oct-1999
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: /note= "C-5 propynl dU"; SEQUENCE DESCRIPTION: SEQ ID NO: 65: US-09-429-130-65
                                                                  Pommier, Eyves
Mazumder, Abhijit
60/015,714
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
Oligonucleotides
NUMBER OF SEQUENCES: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: CURLOWN APPLICATION NUMBER: 60/001,505
FILING DATE: 19-JULY-95
APPLICATION NUMBER: 60/014,007
FILING DATE: 25-MARCH-96
APPLICATION NUMBER: 60/013,688
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 17-APRIL-96
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06214
TELECOMMUNICATION:
                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon,
STREET: 600 Travis, Suite 1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: October 27, 2003, 14:03:36 Job time: 28.5429 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/682,255
   Joseph G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 713/238-8010
TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                            Ojwang, Joshua O.
Hogan, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA
   Zendeguı,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGGTGGTGGG 11
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                                                                                                                                                    NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
STREET: 600 Travis, Suite 1850
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77002-2912
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: MS Word 97 (saved as .txt.file)
Ojwang, Joshua O.
Hogan, Michael E.
Pommier, Eyves
Mazumder, Abhijit
60/015,714
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
Oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06214
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/238-8010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/429,130
FILING DATE: 28-Oct-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/682,255
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: 60/001,505
FILING DATE: 19-JULY-95
APPLICATION NUMBER: 60/014,007
FILING DATE: 25-MARCH-96
APPLICATION NUMBER: 60/013,688
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: 60/013,688
FILING DATE: 17-APRIL-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-APRIL-96
23-APRIL-96
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Patent No. 6355785
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
Fennewald, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GGGTGGTGGGG 13
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US-09-429-130-65
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2422, Ap
2423, Ap
2133, Ap
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2423, Ap
2423, Ap
2423, Ap
39, Appl
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366, Appl
367, App
                                                                       October 27, 2003, 11:25:34; Search time 258.629 Seconds (without alignments) 124.432 Million cell updates/sec
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Sequence
Sequence
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

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17: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
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US-09-740-332-2133
US-09-740-332-2422
US-09-817-879-2132
US-09-817-879-2133
US-09-817-879-2422
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US-09-817-879-2423
US-09-817-879-2423
US-09-817-879-2423
US-09-817-879-2423
US-09-7148-687-39
US-10-184-085A-365
US-10-184-085A-366
                                                                                                                                                                                                                                            hits satisfying chosen parameters:
                                                                                                                                                                                                                     1792395 segs, 1340900451 residues
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Maximum Match 100%
Listing first 45 summaries
                                                  nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 22
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Perfect score:
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Sequence 2132, Application US/09740332

Sequence 2132, Application US/09740332

Publication No. US20030125270A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals Inc.

TITLE OF INVENTION: Hepatitis C virus Infection

TITLE OF INVENTION: Hepatitis C virus Infection

FILE REFERENCE: RPI 400/003

CURRENT APPLICATION NUMBER: US/09/740,332

CURRENT FILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 9704

SOFTWARE: Patentin version 3.0

SEQ ID NO 2132

LENGTH: 17
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TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
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Pred. No. 9e+03;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2132
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US-09-740-332-2133/c
; Sequence 2133, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Ir
; TITLE OF INVENTION: Enzymatic Nucleic
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ilarity 100.0%;
Conservative 0;
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ORGANISM: artificial sequence
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Best Local Similarity
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Sequence 2133, Application US/09817879
Publication No. US20030171311A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT PILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
SEQ ID NO 2133
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                        US-09-817-879-2132/c
; Sequence 2132, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relatering Prints OF INVENTION: Hepatitis C Virus Infection
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MBHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: Patentin version 3.0
; SEQ INC.
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                                                                                                                                                     ch 100.0%; Score 12; DB 11; 1 Similarity 83.3%; Pred. No. 9e+03; 10; Conservative 2; Mismatches 0;
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; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2133
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US-09-817-879-2132
                                             NAME/KEY: misc_feature;
LOCATION:
COTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2423
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Pred. No.
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     ORGANISM: artificial sequence
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Best Local Similarity
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Best Local Similarity
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Matches 10
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TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate TITLE OF INVENTION: Hepatitis C Virus Infection FILE REFERENCE: RPI 400/003
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT PILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: Patentin version 3.0
SEQ ID NO 2423
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US-09-740-332-2422
; Sequence 2422, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Hepatitis C Virus Infection
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/083
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2422
; LENGTH: 17
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Pred. No. 9e+03;
2; Mismatches 0;
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TITLE OF INVENTION: Hepatitis C Virus Infection FILE REFERENCE: RPI 400/003
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: Patentin version 3.0
SEQ ID NO 2133
LENGTH: 17
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                                                                                                                                                                                                                                                                      LOCATION:
; OTHER INFORMATION: oligonucleotide substrate US-09-740-332-2133
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83.38; P
                                                                                                                                                                                TYPE: RNA
ORGANISM: artificial sequence
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Best Local Similarity 83.3
Watches 10; Conservative
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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US-09-740-332-2423
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Sequence 56, Application US/09779152

Publication No. US20030044782A1

GENERAL INFORMATION:

APPLICANT: Acton, Susan L.

APPLICANT: Ordovas, Jose M.

TITLE OF INVENTION: DARBONSTIC ASSAYS AND KITS FOR BODY MASS AND

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS

FILE REFERENCE: MNI-172CP2

CURRENT APPLICATION NUMBER: US/09/779,152

CURRENT APPLICATION NUMBER: 08/890,979

PRIOR FILING DATE: 1997-07-10

NUMBER OF SEQ ID NOS: 121

SOFTWARE: Patentin Ver. 2.0

LENGTH: 20
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                               GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: WILLIAMS, Keith Leslie

APPLICANT: WILLIAMS, Keith Leslie

APPLICANT: WILLIAMS, Keith Leslie

APPLICANT: GOOLEY, Andrew Arthur

APPLICANT: GOOLEY, Andrew Arthur

APPLICANT: GOOLEY, Andrew Arthur

APPLICANT: Cryptosporidium sporozoite antigens

ITILE OF INVENTION: Cryptosporidium sporozoite antigens

FILE REFERENCE: 047763-5019-US

CURRENT APPLICATION NUMBER: US/10/148,687

CURRENT FILING DATE: 2002-05-31,

PRIOR FILING DATE: 1999-12-01

NUMBER OF SEQ ID NOS: 67

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 39

LINGTH: 19
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COTHER INFORMATION: Oligonucleotide primers
US-10-148-687-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 11; DB 11; I Pred. No. 2.5e+04;
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100.0%; Pred. No. ...
0; Mismatches
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Sequence 39, Application US/10148687
Publication No. US20030185836A1
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 11, Conservative
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CRGANISM: Human
US-09-779-152-56
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                                                                                                                                                                                 Sequence 2422, Application US/09817879
Publication WS0030171311A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Hepatitis C virus Infection
FILE REFERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT APPLICATION NUMBER: 12/09/817,879
CURRENT APPLICATION NUMBER: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2422
LENGTH: 17
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; Sequence 2423, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Hepatitis C virus Infection
; TITLE OF INVENTION: Hepatitis C virus Infection
; FILE REFERENCE: MBHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: Patentin version 3.0
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 0; Gaps
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 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: OTHER INFORMATION: Oligonucleotide substrate
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
ORGANISM: artificial sequence
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Best Local Similarity 83.3
Matches 10; Conservative
12; Conservative
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                                            1 GGGGTGGTGGGG 12
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NAME/KEY: misc_feature
LOCATION:
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                                                                                                                                                                        US-09-817-879-2422
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US-10-148-687-39/c
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LENGTH: 17
Matches
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US-10-14-085A-368/C

Squence 368, Application US/10184085A

Publication No. US20030152950A1

GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Minna, John D.
APPLICANT: Luebke, Kevin, J.
APPLICANT: Balog, Robert P.
TITLE OF INVENTION: Identification of Chemically Modified Polymers
FILE REFERENCE: 119929-1035
CURRENT APPLICATION NUMBER: US/10/184,085A

CURRENT FILING DATE: 2002-10-01

PRIOR PAPLICATION NUMBER: US 60/301,370

PRIOR PRILING DATE: 2001-06-27

NUMBER OF SEQ ID NOS: 1291

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 368

LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 367, Application US/10184085A; bublication No. US20030152950A1; bublication No. US20030152950A1; GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Minna, John D.
APPLICANT: Balog, Robert P.
TITLE OF INVENTION: Identification of Chemically Modified Polymers; FILE REFERENCE: 119929-1035; CURRENT APPLICATION NUMBER: US/10/184,085A; CURRENT FILING DATE: 2002-10-01; PRIOR FILING DATE: 2001-06-27; NUMBER OF SEQ ID NOS: 1291; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 367; LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.7%; Score 11; DB 12; Length 21; 100.0%; Pred. No. 2.5e+04; Live 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.5e+04;
cive .0, Mismatches 0;
      PRIOR APPLICATION NUMBER: US 60/301,370
PRIOR FILING DATE: 2001-06-27
NUMBER OF SEQ ID NOS: 1291
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 366
LENGTH: 21
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) TYPE: DNA
) ORGANISM: Homo sapiens
US-10-184-085A-367
                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-10-184-085A-366
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Matches 11; Conserv
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US-10-184-085A-367/c
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GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Minna, John D.
APPLICANT: Luebke, Kevin, J.
APPLICANT: Balog, Robert P.
TITLE OF INVENTION: Identification of Chemically Modified Polymers
FILE REFERENCE: 119929-1035
CURRENT APPLICATION NUMBER: US/10/184,085A
CURRENT APPLICATION NUMBER: US 60/301,370
PRIOR APPLICATION NUMBER: US 60/301,370
PRIOR APPLICATION NUMBER: US 60/301,370
PRIOR FILING DATE: 2002-10-01
SPRIOR FILING DATE: 2002-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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US-10-184-085A-366/c
; Sequence 366, Application US/10184085A
; Publication No. US20030152950A1
; GENERAL INFORMATION:
; APPLICANT: Minna, John D.
; APPLICANT: Luebke, Kevin, J.
; APPLICANT: Balog, Robert P.
; TITLE OF INVENTION: Identification of Chemically Modified Polymers
; FILE REFERENCE: 119929-1035
; CURRENT APPLICATION NUMBER: US/10/184,085A
; CURRENT FILING DATE: 2002-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
APPLICANT: Acton, Susan L.

TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
FILE REFERENCE: MIA-005.03
CURRENT APPLICATION NUMBER: US/10/023,610
CURRENT FILING DATE: 2001-12-17
EARLIER APPLICATION NUMBER: 09/686,106
EARLIER APPLICATION NUMBER: 09/686,106
EARLIER APPLICATION NUMBER: 09/032,894
EARLIER APPLICATION NUMBER: 09/032,894
EARLIER FILING DATE: 1998-02-27
EARLIER PILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin Ver. 2.0
LENGTH: 20
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Pred. No. 2.5e+04;
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100.0%;
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Best Local Similarity 100.
Matches 11; Conservative
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CRGANISM: Homo sapiens
US-10-184-085A-365
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US-10-184-085A-365/c
                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Human
US-10-023-610-56
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Search completed: October 27, 2003, 19:00:53 Job time : 258.629 secs

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Sequence 3, Appli
Sequence 13, Appl
Sequence 49, Appl
Sequence 49, Appl
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                    US-09-331-204-3
US-09-331-204A-13
PCT-US01-21306-49
PCT-US01-21306-49
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19: /cgn2 6/ptodata/1/pna/USO9_COMB.seq:*
10: /cgn2 6/p
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                 October 27, 2003, 10:32:35 ;
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Maximum Match 100%
Listing first 45 summaries
                                                                                    - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                         IDENTITY NUC Gapoxt 1.0
                                                                                                                                                                                                                  US-09-331-204A-13
12
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Perfect score:
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Sequence 2132, Ap Sequence 2423, Ap Sequence 10, Appli Sequence 17, Appli Sequence 42, Appli Sequence 64788, Ap Sequence 64788, Ap Sequence 64788, Appli Sequence 64788, Appli Sequence 21313, Appli Sequence 21313, Appli Sequence 64788, Appli Sequence 2001, Appli Sequence 2001, Appli Sequence 6, Appli Sequence 2001, Ap Sequence 72837, Ap Sequence 72837, Ap Sequence 72837, Ap Sequence 72837, Ap Sequence 78761, Appli 24761, Ap Sequence 78761, Ap Sequence 78837, Appli 2411, Ap Sequence 78761, Ap Sequence 78761, Appli 2411, Ap Sequence 78761, Appli 2411, Appli 24111, Appli 2411, Appli 2411, Appli 2411, Appli 2411, Appli 2411
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Sequence 48, Appl
Sequence 62, Appl
Sequence 64, Appl
Sequence 62, Appl
Sequence 64, Appl
Sequence 64, Appl
Sequence 65, Appl
Sequence 65, Appl
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| Sequence 3, Application US/09331204
| GENERAL INFORMATION:
| APPLICANT: Tam, Robert
| TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
| TITLE OF INVENTION: IMMUNE RESPONSE
| FILE REFERENCE: ICNSequence
| CURRENT APPLICATION NUMBER: US/09/331,204
| CURRENT FILING DATE: 1997-08-20
| PRIOR APPLICATION NUMBER: PCT/US97/23927
| PRIOR FILING DATE: 1997-12-19
| NUMBER OF SEQ ID NOS: 6
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 3
| LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 12; DB 19; Length 12; 100.0%; Pred. No. 8.7e+04;
2 US-09-740-332-2132
2 US-09-740-332-2133
2 US-09-740-332-2133
4 US-09-740-332-2422
4 US-09-740-332-2422
4 US-09-817-879-2423
4 US-09-817-879-2423
6 US-09-817-879-2423
6 US-09-817-879-2423
7 US-09-331-204A-6
7 US-10-310-188-78501
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Best Local Similarity
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RESULT 2
US-09-331-204A-13
Sequence 13, Application US/09331204A
Sequence 13, Application US/09331204A
Sequence 13, Application US/09331204A
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
Grich Oligo Aptamers and Methods of Modulating an Immune Resp.
TITLE OF INVENTION:
TITLE OF INVENTION:
GOVERNOR:
CURRENT FILING DATE: 1999-08-20
FRIOR APPLICATION NUMBER: PCT/US97/23927
FRIOR APPLICATION NUMBER: PCT/US97/23927
NUMBER OF SEQ ID NOS: 28
SOFTWARE:
SEQ ID NO 13
LENGTH: 12
LENGTH: 12
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APPLICANT: Genaissance Pharmaceuticals, Inc.
APPLICANT: Benaissance Pharmaceuticals, Inc.
APPLICANT: Bieglecki, Karyn M.
APPLICANT: Kazemi, Amir
APPLICANT: Kazemi, Amir
APPLICANT: Koshy, Beena
TITLE OF INVENTION: Haplotypes of the ETFB Gene
TITLE OF INVENTION: Haplotypes of the ETFB Gene
TITLE OF INVENTION WIMBER: PCT/US01/21306
CURRENT FILING DATE: 2001-07-06
PRIOR PILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 141
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 49
Mismatches
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PCT-US01-21306-49
Sequence 49, Application PC/TUS0121306
GENERAL INFORMATION:
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Best Local Similarity 100...
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12; Conservative
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; ORGANISM: Homo sapiens
PCT-US01-21306-49
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APPLICANT; Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relail TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: RPI 400/003
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: Patentin version 3.0
SEQ ID NO 2423
LENGTH: 17
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TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relations Intle OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: RPI 400/003
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: Patentin version 3.0
SEQ ID NO 2422
LENGTH: 17
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100.0%; Score 12; DB 32;
Best Local Similarity 83.3%; Pred. No. 8.7e+04;
Matches 10; Conservative 2; Mismatches 0;
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         CRGANISM: artificial sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION:
CTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2133
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ORGANISM: artificial sequence
FEATURE:
NAME/KEY: misc_feature
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US-09-740-332-2422
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TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: RPI 400/003
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2133
LENGTH: 17
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TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: RPI 400/003
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: Patentin version 3.0
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APPLICANT: Bentivegna, Steven C
APPLICANT: Bieglecki, Karyn M.
APPLICANT: Kazemi, Amir
APPLICANT: Kashy, Beena
TITLE OF INVENTION: Haplotypes of the ETFB
CURRENT APPLICATION NUMBER: PCT/US01/21306
CURRENT FILING DATE: 2001-07-06
PRIOR FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 141
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 12; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 8. Matches 12; Conservative 0; Mismatches
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US-09-740-332-2133/c
; Sequence 2133, Application US/09740332
; GENERAL INFORMATION:
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ORGANISM: artificial sequence
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; ORGANISM: Homo sapiens
PCT-US01-21306-49
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Sequence 2423, Application US/09817879

Sequence 2423, Application US/09817879

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals Inc.

TITLE OF INVENTION: Bepatitis C Virus Infection

TITLE OF INVENTION: Hepatitis C Virus Infection

FILE REFERENCE: MBH800-801-F

CURRENT APPLICATION NUMBER: US/09/817,879

CURRENT FILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 9703

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2423

LENGTH: 17
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GENERAL INFORMATION:
APPLICANT: RosettaGenomics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
FILE REFERENCE: 47416
CURRENT APPLICATION NUMBER: US/10/303,778
CURRENT APPLICATION NUMBER: 2002-11-26
NUMBER OF SEQ ID NOS: 17608
SOFTWARE: Patentin version 3:1
SEQ ID NO 13820
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83.3%; Pred. No. 8.7e+04;
live 2; Mismatches 0;
       Hepatitis C Virus Infection
                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: oligonucleotide substrate US-09-817-879-2422
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TITLE OF INVENTION: Hepatitis C Virus Inf
FILE REFERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2422
LENGTH: 17
                                                                                                                                                                                     TYPE: RNA
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: RNA ORGANISM: artificial sequence
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Best Local Similarity 83.3'
Matches 10; Conservative
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Best Local Similarity 83.3
Matches 10; Conservative
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US-10-303-778-13820
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; ORGANISM: Homo :
US-10-303-778-13820
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US-09-817-879-2423
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APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
SEQ ID NO 2132
LENGTH: 17
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GENERAL INFORMATION:
APPLICANT: RICORMATION:
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
SEQ ID NO 2133
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
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LOCATION:
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us-09-331-204a-13.szlm22.rnpm

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COMPUTER READABLE FORM:
MEDIUM TYPE: IPOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,041A
FILING DATE: 02-FEB-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 6250-011
TELEPHONE: 415-854-366
TELEFAX: 415-854-369
TELEPHONE: 415-854-369
TELEFAX: 66141 PENNE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 12;
100.0%; Pred. No.
ative 0; Mismatch
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Job time : 1570.86 secs
United States of America
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Best Local Similarity 100.
Matches 12; Conservative
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| Sequence 10, Application US/08387041A
| GENERAL INFORMATION:
| APPLICANT: Tam, Robert C. |
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION |
| TITLE OF INVENTION: OF CD28 EXPRESSION |
| NUMBER OF SEQUENCES: 41 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Pennie & Edmonds |
| STREET: 1155 Avenue of the Americas |
| CITY: New York
              Query Match 100.0%; Score 12; DB 50; Length 17; Best Local Similarity 100.0%; Pred. No. 8.7e+04; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 8; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/387,041A

FILING DATE: 02-FEB-1995

CLASSIFICATION: S14

ATTORNEY/AGENT INFORMATION:

NAME: Hallun, Albert P:

REFERENCE/DOCKET NUMBER: 25,227

REFERENCE/DOCKET NUMBER: 8250-011

TELEPHONE: 415-854-3660

TELEPHONE: 415-854-3694

TELEPHONE: 415-884-3694

TELEPAX: 415-884-3694

TELEPAX: 611 PENNIE

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

LENGTH: 18 base pairs
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Best Local Similarity 100.
Matches 12; Conservative
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Length 18;

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
OM nucleic - nucleic search, using sw model
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 Run on:
 October 27, 2003, 11:09:34; Search time 204.686 Seconds (without alignments)

 97.777 Million cell updates/sec

 Title:
 US-09-331-204A-13

 Perfect score:
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 Sequence:
 1 9999t99t99g12

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched: 2231628 segs, 833900706 residues
Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 22 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database: Pending Patents NA New:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7861 Sequence 57870, 12 100.0 21 PCT-USO2-38216-72837 Sequence 57870 Sequence 57870, 12 100.0 22 1 PCT-USO2-38216-72837 Sequence 57870, 12 100.0 22 1 PCT-USO2-38216-10573 Sequence 57870, 13 1 PCT-USO2-38216-10573 Sequence 57870, 14 19 1.7 18 1 PCT-USO2-38216-3329 Sequence 57870, 16 1 PCT-USO2-38216-10573 Sequence 57870, 17 19 1 PCT-USO2-38216-10573 Sequence 57870, 17 19 1 PCT-USO2-38216-10573 Sequence 786870, 17 10 PCT-USO2-38216-10573 Sequence 57870, 17 10 PCT-USO2-38216-10573 Sequence 67021 PCT-USO2-38216-10564 Sequence 67021 PCT-USO2-38216-10564 Sequence 67021 PCT-USO2-38216-64021 Sequence 67021 PCT-USO2-38216-64021 Sequence 67021 PCT-USO2-38216-64021 Sequence 67021 PCT-USO2-38216-64021 Sequence 67021 PCT-USO2-38216-64022 Sequence 64021 PCT-USO2-38216-10564 PCT-USO2-38216-10564 PCT-USO2-38216-10564 PCT-USO2-38216-10564 PCT-USO2-38216-10564 PCT-USO2-382

Sequence 2, Appli Sequence 39252, A	equence 63970, .	83087,	e 34808,	72787,	equence 84942,	84968,	9718, A	equence 31332,	51833,	eguence 60635,	61028,	e 64024,	equence 72823,	e 73073,	nce 75530,	e 9811, A	e 26671,
25	-US02-38216-63	-US02-38216-8308			-US02-38216-8494	PCT-US02-38216-84968	-US02-38216-971	216-3133	PCT-US02-38216-51833	-US02-38216-6063	16-6102	6-6402	-US02-38216-7282	PCT-US02-38216-73073	16-755	216-9	16-26
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ALIGNMENTS

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Sequence 4725, Application US/10669841
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APPLICANT: Barrance. Blate the APPLICANT Denies, McCayage
APPLICANT: Denies, McCayage
APPLICANT: Partice between the APPLICANTON WINGHOUSE TO SEPTICANTON WINGHOLD THE SEPTICANTON WINGHOLD THE SEPTICANTON WINGHER: US/0669,841
CURRENT PAPLICATION WINGER: US/069.28
FILE OF INVENTION: OLICOMOLOGICAL SOUTH SEPTICATION WINGER: US/0669,841
CURRENT PAPLICATION WINGER: US/069.28
FILE SEPTICATION WINGER: US/069.28
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FILE SEPTICATION WINGER: US/069.39
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APPLICANT: Panela, MOSTISSEY
APPLICANT: Panela, MOSTISSEY
APPLICANT: Panela, Pavco
APPLICANT: Panela, Pavco
APPLICANT: Patrice, Lee
APPLICANT: Elsabeth, Roberts
APPLICANT: Elsabeth, Roberts
TITLE OF INVENTION: OLIGONUCLECATION MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HE
TITLE OF INVENTION: VIRUS REPLICATION
FILE SEPERENCE: 400/0420S (MRHB02-249-E)
CURRENT FILING DATE: 2003-09-23
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
PRIOR PELING DATE: 2001-06-08
PRIOR PLING DATE: 2001-06-08
PRIOR PLING DATE: 2001-06-08
PRIOR PLING DATE: 2001-06-08
PRIOR PLING DATE: 2001-03-26
PRIOR PLING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 09/41,332
PRIOR PLING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 09/40,332
PRIOR PLING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 09/504,321
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PRINK DATE: 2000-07-07
PRIOR PRINK DATE: 2000-07-07
PRIOR PLING DATE: 2000-02-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Remaining DATE: 2000-02-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 16207
SOFTWARE: Patentin version 3.0
SEQ ID NO 5015
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2; Mismatches 0; Indels
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; COTHER INFORMATION: oligonucleotide substrate
US-10-669-841-5015
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                                                                       Sequence 5015, Application US/10669841
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sirna Therapeutics, Inc. APPLICANT: Lawrence, Blatt APPLICANT: Dennis, Macejak APPLICANT: James, McSwiggen APPLICANT: David, Morrissey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                    Dennis, Macejak
James, McSwiggen
David, Morrissey
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Best Local Similarity 83.3
Matches 10, Conservative
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                                                                         Query Match
100.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
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; LOCATION:
; OTHER INFORMATION: oligonuclectide substrate
US-10-669-841-4725
                                                                                                                                                                                                                                                    RESULT 2
US-10-669-841-4726/c
; Sequence 4726, Application US/10669841
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sirna Therapeutics, Inc. APPLICANT: Lawrence, Blatt APPLICANT: Dennis, Macejak APPLICANT: James, McSwiggen APPLICANT: David, Morrissey
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGGTGGTGGGG 12
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Sequence 46976, Application PC/TUS0238216

Sequence 46976, Application PC/TUS0238216

GENERAL INFORMATION:

APPLICANT: Rosetta Genomics LTD

TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY

TITLE OF INVENTION: GENES AND USES THEREOF

FILE REFERENCE: 55002

CURRENT APPLICATION NUMBER: PCT/US02/38216

CURRENT FILING DATE: 2002-11-12

CURRENT FILING DATE: 2002-11-12

SOFTWARE: Patentin version 3.2

SEQ ID NO 46976

LENGTH: 19
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PCT-US02-38216-72857
; Sequence 72857, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: ROSetta Genomics LTD
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 72857
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; Sequence 64788, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
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Pred. No. 1.4e+04;
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Best Local Similarity 100.
Matches 12; Conservative
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Matches 12; Conservative
  Conservative
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; ORGANISM: Homo sapiens
PCT-US02-38216-72857
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; ORGANISM: Homo sapiens
PCT-US02-38216-46976
  12;
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Matches
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     APPLICANT: Pararie, reance, reavoon APPLICANT: Renneth, Drager
APPLICANT: Renneth, Drager
APPLICANT: Renneth, Drager
APPLICANT: Elisabeth, Roberts
APPLICANT: Elisabeth, Roberts
APPLICANT: Elisabeth, Roberts
TITLE OF INVENTION: UTING STREPLICATION
TITLE OF INVENTION: UTING STREPLICATION
TILE OF INVENTION: UNMER: US/10/669,841
CURRENT APPLICATION NUMBER: US/10/669,841
CURRENT FILING DATE: 2002-09-23
PRIOR PILING DATE: 2002-09-23
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
PRIOR PILING DATE: 2001-10-24
PRIOR PILING DATE: 2001-10-24
PRIOR PILING DATE: 2001-03-26
PRIOR PILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
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PRIOR PILING DATE: 2000-03-26
PRIOR PILING DATE: 2000-03-26
PRIOR PILING DATE: 2000-03-26
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR PILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR PILING DATE: 2000-02-15
PRIOR PILING DATE: 2000-03-16
PRIOR
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: GENES AND USES THEREOF
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NOS: 86841
SEQ ID NOS: 86841
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Pred. No. 1.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: oligonucleotide substrate US-10-669-841-5016
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ORGANISM: Artificial Sequence
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CORGANISM: Homo sapiens
PCT-US02-38216-9770
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Best Local Similarity
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PCT-USIZ-38216-72837

Sequence 72837, Application PC/TUS0238216

GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
LENGTH: 21
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 31329
LENGTH: 21
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Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                              100.0%; Score 12; DB 1; Length 21; 100.0%; Pred. No. 1.3e+04; ive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0;
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; ORGANISM: Homo sapiens
PCT-US02-38216-78761
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; ORGANISM: Homo sapiens
PCT-US02-38216-72837
                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
PCT-US02-38216-31329
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Best Local Similarity
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PCT-US02-38216-78761
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; Sequence 78501, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: ROSELTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.2
; SOFTWARE: Patentin version 3.2
; SOFTWARE: Patentin version 3.2
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GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 31313
LENGTH: 20
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                                                                                                                                    Ouery Match 100.0%; Score 12; DB 1; Length 19; Best Local Similarity 100.0%; Pred. No. 1.4e+04; Matches 12; Conservative 0; Mismatches 0; Indels
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PCT-US02-38216-31329
; Sequence 31329, Application PC/TUS0238216
; GENERAL INFORMATION:
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CORGANISM: Homo sapiens
PCT-US02-38216-78501
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; ORGANISM: Homo sapiens
PCT-US02-38216-31313
                                                TYPE: DNA
CORGANISM: Homo sapiens
PCT-US02-38216-64788
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PCT-US02-38216-31313
       SEQ 1D NO 64788
                                 LENGTH: 19
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Matches
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Sequence 78761, Application PC/TUS0238216

Sequence 78761, Application PC/TUS0238216

GENERAL INFORMATION:

APPLICANT: ROSetta Genomics LTD

TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY

TITLE OF INVENTION: GENES AND USES THEREOF

FILE REFERENCE: 55002

CURRENT APPLICATION NUMBER: PCT/US02/38216

CURRENT FILING DATE: 2002-11-12

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: Patentin version 3.2

SOFTWARE: Patentin version 3.2
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Sequence 42141, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 42141
LENGTH: 22
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Sequence 39287, Application PC/TUS0238216
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 39287
LENGTH: 17
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Best Local Similarity 100.
Matches 11; Conservative
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CORGANISM: Homo sapiens
PCT-US02-38216-42141
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CORGANISM: Homo sapiens
PCT-US02-38216-39287
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PCT-US02-38216-39287
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PCT-US02-38216-42141
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Nucleotide sequenc Triplex forming ol CD28 inhibiting ph CD28 inhibition ol Gastric acid produ Hammerhead ribozym Rat PTPIB antisens Rat PTPIB antisens Rat PTPIB antisens Rat PTPIB mRNA lev MMy24 nucleotide c Human POSHL1 scann Human POSHL1 scann Human POSHL1 scann Human POSHL1 scann Human DOSHL1 scann Human DOSHL1 scann Human DOSHL1 scann Frimer ON-DHFR-F1 Human DOSHL1 scann CD28 expression in CD28 inhibiting ph Hepatitis C virus Human CC3 promoter Triple helix formi Human Lissue kalli Human Lissue kalli Human Lissue kalli Primer for breast C. glutamicum ATCC Human GLCLA gene e Rat PTPIB antisens Rat PTPIB mRNA lev Primer used when o Primer used when o

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Reduction; T cell; CD28; gene expression; treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; psoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2; systemic lupus erythematosus; inflammatory bowel disease; IL-2; production; antisense; inhibition; ss
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ABK99294
ABT08387
AAX14740
AAV55680
AAV55680
AAK00094
AAL43484
AAL43484
AAL49336
AAK37362
AAK06186
AAZ99650

AAT36197

AAX90329

AAX90291

AAF16593

AAF1021157

ABK37361

AAC06932

ABK37361

AAC06932

AAT98040

ABK91221

AAC91221

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95US-0529878.
95US-0387041.
95US-0529878.
   96WO-US01507
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(first entry)
   09-FEB-1995;
18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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16-APR-1997
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  Synthetic.
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                                                                                                      ; Search time 162 Seconds (without alignments) 299.938 Million cell updates/sec
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2. /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3. /SIDS1/gcgdata/geneseqn-embl/NA1982.DAT:*
4. /SIDS1/gcgdata/geneseqn-embl/NA1983.DAT:*
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6. /SIDS1/gcgdata/geneseqn-embl/NA1983.DAT:*
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22. /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
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22. /SIDS1/gcgdata/geneseqn-embl/NA2001B.DAT:*
23. /SIDS1/gcgdata/geneseqn-embl/NA2001B.DAT:*
24. /SIDS1/gcgdata/geneseqn-embl/NA2001B.DAT:*
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                5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                          2552756 segs, 1349719017 residues
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                 GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AAX90336
AAT36242
AAT36196
AAX90328
AAX90290
AAX90290
                                                                           nucleic search, using sw model
                                                                                                        October 27, 2003, 10:32:29
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Match Length
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length: 22
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Result No.

Human promoter

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AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reduction; T cell; CD28; gene expression; treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; psoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2; systemic lupus erythematosus; inflammatory bowel disease; IL-2; production; antisense; inhibition; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
                                                                                                                                                                                                      .
                                                                                                                                                            Length 18;
                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD28 expression inhibiting oligonucleotide, RT05s.
                                                                                                                                                            100.0%; Score 18; DB 20; 100.0%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                      Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;
                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 45; 77pp; English.
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95US-0529878.
95US-0387041.
95US-0529878.
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                                                                                                                                                                                                                                                                                                                                                                                     AAT36242 standard; DNA; 18
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(first entry)
                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ICNC ) ICN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-384228/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytokine release
                                                                                 present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
16-APR-1997
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AAT36242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                      (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated disease, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD28; inhibition, antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8;
                                                                                                     for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
                                                                                                                                                                                                                                           The present oligonucleotide reduces CD28 dependent interleukin-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD28 inhibiting phosphorothioate oligonucleotide RT09S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 18; DB 17;
100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;
                                                                                                                                                                                                    Example 2; Page 45; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Column 24; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TTGGAGGGGGAGGTGGGG 18
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 (ICNC ) ICN PHARM INC
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-443609/37.
                                                                                 WPI; 1996-384228/38
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Matches

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The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN).

AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonucleotide used in the exemplification of the
                                                                                                                                                                                             CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; phosphorothicate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD28 inhibiting phosphorothioate oligonucleotide RT05S.
                                                                                                                                                            CD28 inhibiting phosphorothioate oligonucleotide RT03S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.1%; Score 16.4; DB 20;
94.4%; Pred. No. 1.4e+03;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
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                                                         ВР.
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                                                                                                                             (first entry)
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les 17; Conservative
                                                         AAX90328 standard; DNA;
                                                                                                                                                                                                                immune system mediate phosphorothioate; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                          (TAMR/) TAM R
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                                                                                          AAX90328;
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                        RESULT 5
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                                      AAX90328
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                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                Reduction, T cell, CD28; gene expression; treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; psoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR; systemic lupus erythematosus; inflammatory bowel disease; triplex forming; oligonucleotide; 5'-untranslated region; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present oligonucleotide reduces T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligo:nucleotide which reduces CD28 gene expression in T cells - for treating immune system disease, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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     Length 18;
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Pred. No. 1.4e+03;
0; Mismatches 1;
     DB 17;
    Score 16.4; DB 17;
Pred. No. 1.4e+03;
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                                      Mismatches
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95US-0529878.
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Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                        TTGGAGGGGGAGGAGGG
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(first entry)
                     Similarity 94.4 17; Conservative
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09-FEB-1995;
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15-APR-1997
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Query Match
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The present sequence represents a G-motif oligonucleotide of the invention. The specification describes compositions comprising G-motif oligonucleotides inhibit activation of antigen presenting cells by inhibiting the uptake of DNA by a cell, by stimulating natural killer cells, or by co-stimulating cytotoxic T-lymphocytes. The G-motif oligonucleotides may be used for the productions of vaccines for treating septic shock, inflammation, autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease, sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host disease and transplant rejection), helper T cell response 1-mediated diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic inflammatory bowel disease, psoriasis vulgaris, experimental allergic
The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection; antigen presenting cell activation; natural killer cell; septic shock; cytotoxic T-lymphocyte; inflammation; autoimmune disease; rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis; Kawasaki syndrome; graft-versus-host disease; transplant rejection; helper T cell response 1-mediated disease; Lyme arthritis; streptococcal induced arthritis; chronic inflammatory bowel disease; psoriasis vulgaris; experimental allergic encephalomyelitis; insulin-dependent diabetes mellitus; bacterial infection; tumour; ss. parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.
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                                                                                                                                                                                      Score 16.4; DB 20;
Pred. No. 1.4e+03;
0; Mismatches 1;
                                                                                                                                               Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
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Best Local Similarity 94.4'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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AAX90290 RESULT

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encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis), viral infections (e.g. Cytomegalovirus and human immunodeficiency virus (HIV) -infections), spontaneous abortions and tumours. They may also be used to induce proliferation of bone marrow cells, especially macrophage precursor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a non-G-motif oligonucleotide of the invention. The specification describes compositions comprising G-motif oligonucleotides inhibit activation of antigen presenting cells by inhibiting the uptake of DNA by a cell, by stimulating natural killer cells, or by co-stimulating cytotoxic T-lymphocytes. The G-motif oligonucleotides may be used for the productions of vaccines for treating septic shock, inflammation, autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease, sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host disease and transplant rejection), helper T cell response 1-mediated diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic inflammatory bowel disease, psoriasis vulgaris, experimental allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G-motif oligonucleotide, vaccine, Toxoplasmosis; viral infection, antigen presenting cell activation; natural killer cell; septic shock; cytotoxic T-lymphocyte; inflammation; autoimmune disease, rheumatoid arthritis; Crohn's disease, sarcoidosis; multiple sclerosis; Kawasaki syndrome, graft-versus-host disease, transplant rejection; helper T cell response 1-mediated disease; Lyme arthritis; Streptococcal induced arthritis; chronic inflammatory bowel disease; psoriasis vulgaris; experimental allergic encephalomyelitis; insulin-dependent diabetes mellitus; bacterial infection; tumour; ss.
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                                                                                                                                                                    Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence of non-G-motif oligonucleotide GRF1comp.
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                                                                                                                                                                 Score 16.4; DB 21;
Pred. No. 1.4e+03;
0; Mismatches 1;
                                                                                                                                Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
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Matches 17; Conserv
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encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis), viral infections (e.g. Cytomegalovirus and human immunodeficiency virus (HIV)-infections), spontaneous abortions and tumours. They may also be used to induce proliferation of bone marrow cells, especially macrophage precursor cells.
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reduction; T cell; CD28; gene expression; treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; psoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR; systemic lupus erythematosus; inflammatory bowel disease; triplex forming; oligonucleotide; 5'-untranslated region; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present oligonucleotide reduces T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
(Updated on 25-MAR-2003 to correct PR field.)
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host disease,
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stem diseases, e.g. graft vs.
                                                                                                                                           Score 16.4; DB 21;
Pred. No. 1.4e+03;
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for treating immune system di
septic shock, psoriasis, etc.
                                                                                                                Sequence 18 BP; 4 A; 13 C; 0
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94.4%;
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(first entry)
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Best Local Similarity 94.4<sup>5</sup>
Whiches 17; Conservative
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15-APR-1997
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Query Match 91.1%; Best Local Similarity 94.4%; Matches 17; Conservative

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AAX90329 standard; DNA; 21

RESULT 11

(first entry)

24-SEP-1999

AAX90329;

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The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.
                             CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gastric acid disturbance, gastric reflux, gastritis, dyspepsia, stomach ulcer, duodenal ulcer, Helicobacter pylori, antisense, DNA-RNA hybrid, ss.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gastric acid production inhibiting oligonucleotide SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 21;
                                                                                                                                                                                                                                                                                                                                             Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 94.4%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
CD28 inhibition oligonucleotide RT04
                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Column 29; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TTGGAGGGGAGGTGGGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
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                                                                                                                                                                               95US-0529878
                                                                                                                                                                                                                 95US-0529878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF16593 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                WPI; 1999-443609/37.
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                                                                                                                                                                                                                                             (TAMR/) TAM R C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200071164-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAR-2001
                                                                                                                                                                                18~SEP-1995;
                                                                                                                                                                                                                 18-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-NOV-2000
                                                                                                              US5932556-A
                                                                                                                                                03-AUG-1999
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                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tachas G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF16593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases.
                                                                                                                                                                                                                                                                             Tam RC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                  IL-2;
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                 Length 21;
                                                                                                                                                                                                                                                                                                                                  .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                       CD28; inhibition; antisense oligonucleotide; interleukin
immune system mediated disease; gamma-interferon; IL-8;
phosphorothioate; ss.
                                                   Indels
                                                                                                                                                                                                                                                                                                CD28 inhibiting phosphorothioate oligonucleotide RT04S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 91.1%; Score 16.4; DB 20; Best Local Similarity 94.4%; Pred. No. 1.4e+03; Matches 17; Conservative 0; Mismatches 1;
                Score 16.4; DB 17;
Fred. No. 1.4e+03;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
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Example, Column 21, 45pp, English.

WPI; 1999-443609/37

95US-0529878

JS5932556-A 03-AUG-1999

Synthetic

95US-0529878

18-SEP-1995; 18-SEP-1995;

(TAMR/) TAM R C.

ram RC;

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TTGGAGGGGGAGGTGGGG Trechececercerece

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8

present invention.

ВР

AAX90291 standard; DNA; 21

(first entry)

24-SEP-1999

AAX90291;

RESULT 1
AAX90291
ID AAX
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AC AAX
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Length 17;

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Score 14.4; DB 21;
Pred. No. 8.4e+03;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mod_base= OTHER
/note= "Methoxyethyl residues"
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1..20
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/mod_base= m5c
 80.0%;
93.8%;
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                                                                                                                                                                                                 AAD12117 standard; DNA; 20
                                                                                                                                                                                                                                                                       (first entry)
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                                                                       3 GGAGGGGGAGGTGGGG
                                                                                                         16 GGAGGGTAGGTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ъ
Query Match
Best Local Similarity 93.8
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wyatt J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-432181/46.
                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus.
Synthetic.
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                                                                                                                                                                                                                                                                       25-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                              infection;
                                                                                                                                                                                                                                    AAD12117;
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                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                     The present invention provides oligonucleotides, and methods for their use, which are useful in modulating the action of proteins involved in gastric acid production. The target protein is preferably the histamine H2 receptor or one of the proteins which form part of the gastric proton pump. The sequences and methods of the invention are useful in the treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers, duodenal ulcers and other gastric acid disturbances, most of which are caused by Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUF-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition of and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha.
                 Treating gastric acid disturbance by administering an oligonucleotide which modulates the activity of a polypeptide involved in gastric acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribozyme; erythropoietin; granulocyte colony stimulating factor; interferon alpha; ss.
                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                          Length 22;
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                       82.2%; Score 14.8; DB 22;
ilarity 81.2%; Pred. No. 5.8e+03;
Conservative 3; Mismatches 0;
                                                                                                                                                                                                                                                                                      Sequence 22 BP; 0 A; 0 C; 16 G; 3 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 2 A; 12 C; 0 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McSwiggen J;
                                                                                       Example 3; Page 145; 164pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hammerhead ribozyme substrate #249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 37; Page 61; 164pp; English
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D
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGMGGGGGMGGKGGG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-APR-2000; 2000WO-US09721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0129390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF01954 standard; DNA; 17
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                                                                                                                                                                                                                                                                                                                                                                                                 2 TGGAGGGGGAGGTGGG
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                                                       production or secretion
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                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200061729-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF01954;
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
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New antisense compounds capable of modulating expression of human protein phosphatase 1B, useful for diagnosis, prophylaxis and treatment of diseases associated with expression of protein phosphatase
Gaps
                                                                                                                                                                                                 PTP1B; protein phosphatase 1B inhibitor; antisense; gene theraction; inflammation; tumour; prophylaxis; phosphorothioate; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention is directed to antisense compounds, particularly oligonucleotides which are targetted to a DNA encoding protein phosphatase 1B (PTP1B) to modulate its expression. The antisense compounds are useful for diagnosis, prophylaxis and treatment of diseases associated with the expression of PTP1B, to prevent or delay infection, inflammation and tumour formation and as a research reagent. The PTP1B DNA is useful in gene therapy. The present sequence is an antisense oligonucleotide with a
..
O
Indels
                                                                                                                                                                           Rat PTP1B antisense oligonucleotide (ISIS# 113721)
                                                                                                                                                                                                                                                                                                         /mod_base= OTHER
/note= "Phosphorothioate backbone"
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phosphorothioate backbone. This oligo is targetted to rat PTP1B to inhibit its expression. 8 x 8 8

Sequence 20 BP; 2 A; 3 C; 13 G; 2 T; 0 other;

Query Match 76.7%; Score 13.8; DB 22; Length 20; Best Local Similarity 88.2%; Pred. No. 1.4e+04; Matches 15; Conservative 0; Mismatches 2; Indels (

2 TGGAGGGGGAGGTGGGG 18 ||| || || || || || || || || || || 1 1 TGGCCGGGGAGGTGGGG 17

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Search completed: October 27, 2003, 11:25:21 Job time : 163 secs

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                                                                                                                                                                                                                                October 27, 2003, 11:09:34 ; Search time 307.029 Seconds (without alignments) 97.777 Million cell updates/sec
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1. /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

2. /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*

3. /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
                                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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PCT-US02-38216-18159
PCT-US02-38216-18159
PCT-US02-38216-18159
PCT-US02-38216-18239
PCT-US02-38216-6229
PCT-US02-38216-38911
PCT-US02-38216-38912
PCT-US02-38216-38954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2231628 segs, 833900706 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                           - nucleic search, using sw model
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18
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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                                                                                                                                                                                                                                                 Run on:
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Sequence 60884, A Sequence 18290, A Sequence 25803, A Sequence 39021, A Sequence 39021, A Sequence 41601, A Sequence 6296, Ap Sequence 26644, A Sequence 38922, A Sequence 38922, A Sequence 38986, A Sequence 38986, A Sequence 38986, A Sequence 38986, A Sequence 27400, A Sequence 18060, A Sequence 26562, A Sequence 26562, A		VEL VIRAL REGULATORY	0; Gaps 0;	VEL VIRAL REGÚLATORY	0; Gaps 0;
3.4 74.4 17 1 PCT-US02-38216-60884 3.4 74.4 18 1 PCT-US02-38216-18290 3.4 74.4 18 1 PCT-US02-38216-18290 3.4 74.4 18 1 PCT-US02-38216-38927 3.4 74.4 18 1 PCT-US02-38216-39021 3.4 74.4 18 1 PCT-US02-38216-39023 3.4 74.4 19 1 PCT-US02-38216-41601 3.4 74.4 19 1 PCT-US02-38216-6264 3.4 74.4 19 1 PCT-US02-38216-5296 3.4 74.4 20 1 PCT-US02-38216-5998 3.4 74.4 20 1 PCT-US02-38216-5998 3.4 74.4 20 1 PCT-US02-38216-3998 3.4 74.4 20 1 PCT-US02-38216-3998 3.4 74.4 20 1 PCT-US02-38216-3998 3.5 73.3 20 1 PCT-US02-38216-18060 3.5 73.3 20 1 PCT-US02-38216-992 3.7 73.3 22 1 PCT-US02-38216-992	ALIGNMENTS	RESULT 1 PCT-US02-38216-47426 Sequence 47426, Application PC/TUS0238216 GENERAL INFORMATION: APPLICANT: ROSELTA GENOMICS LTD TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL: TITLE OF INVENTION GENES AND USES THEREOF FILE REFERENCE: 55002 CURRENT APPLICATION NUMBER: PCT/US02/38216 CURRENT FILING DATE: 2002-11-12 NUMBER OF SEQ ID NOS: 86841 SEQ ID NO 47426 LENGTH: 19 TYPE: DNA ORGANISM: Homo sapiens PCT-US02-38216-47426	ch 94.4%; Score 17; DB 1; Length 19; Il Similarity 100.0%; Pred. No. 1.8e+03; 17; Conservative 0; Mismatches 0; Indels 2 TGGAGGGGAGGAGGG 18	ESULT 2 CT-US02-38216-6227/C Sequence 6227, Application PC/TUS0238216 GENERAL INFORMATION: APPLICANT: ROSetta Genomics LTD TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL TITLE OF INVENTION: GENES AND USES THEREOF FILE REFERENCE: 55002 CURRENT APPLICATION NUMBER: PCT/US02/38216 CURRENT FILING DATE: 2002-11-12 NUMBER OF SEQ ID NOS: 86841 SOFTWARE: Patentin version 3.2 LENGTH: 18 TYPE: DNA ORGANISM: Homo sapiens CT-US02-38216-6227	atch 83.3%; Score 15; DB 1; Length 18; cal Similarity 100.0%; Pred. No. 9.1e+03; 15; Conservative 0; Mismatches 0; Indels
0 00 0 0000000000000000000000000000000		RESULT 1 PCT-USO2-38 Sequence GENERAL I APPLICAN TITLE OF TITLE OF TITLE OF TITLE OF CURRENT CURRENT CURRENT CURRENT CURRENT TYPE: D D NO SEQ ID NO COGANIS COGANIS COGANIS COGANIS COGANIS COGANIS COGANIS COGANIS COGANIS	Query Matches Matches Qy	RESULT 2 PCT-US02-382; Sequence 6; GENERAL IN APPLICANT TITLE OF TITLE OF FILE REFE CURRENT A CURRENT A CURRENT B SOFTWARE: SOFTWARE: SOFTWARE: TYPE: DN ORGANISM CORGANISM	Query Mat Best Loca Matches

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RESULT 6
PCT-US02-38216-6229/c

Sequence 6229, Application PC/TUS0238216

GENERAL INFORMATION:

APPLICANT: ROSetta Genomics LTD

TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY

TITLE OF INVENTION: GENES AND USES THEREOF

FILE REFERENCE: 55002

CURRENT APPLICATION NUMBER: PCT/US02/38216

CURRENT APPLICATION NUMBER: PCT/US02/38216

CURRENT PILING DATE: 2002-11-12

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: PatentIn version 3.2

LENGTH: 18

LENGTH: 18
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GENERAL INFORMATION:
APPLICANT: ROSELTA GENOMICS LTD
TITLE OF INVENTION: GENES AND USES THEREOF
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 39031
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; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
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93.8%; Pred. No. 1.5e+04;
Live 0; Mismatches 1;
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93.8%; Pred. No. 1.5e+04;
tive 0; Mismatches 1;
                                                                                      80.0%; Score 14.4; DB 1; 93.8%; Pred. No. 1.5e+04;
                                                                                                                               0; Mismatches
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                                                                                Query Match
Best Local Similarity 93.8
Matches 15, Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
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ORGANISM: Homo sapiens
PCT-US02-38216-39031
 ; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-38911
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PCT-US02-38216-41647
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PCT-US02-38216-39032

; Sequence 39032, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: ROSetta Genomics LTD
; TITLE OF INVENTION: BENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 39032
; LENGTH: 16
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Sequence 38911, Application PC/TUS0238216

GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: GENES AND USES THEREOF
TITLE OF INVENTION GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 38911
LENGTH: 17
                                                                                                                    PCT-USO2-38216-18159
) Sequence 18159, Application PC/TUSO238216
) Sequence 18159, Application PC/TUSO238216
) GENERAL INFORMATION:

APPLICANT: Rosetta Genomics LTD

TITLE OF INVENTION: GENES AND USES THEREOF

TITLE OF INVENTION: GENES AND USES THEREOF

CURRENT PAPLICATION NUMBER: PCT/USO2/38216

CURRENT PAPLICATION NUMBER: PCT/USO2/38216

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: Patentin version 3.2

SSEQ ID NO 18159
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88.9%; Pred. No. 1.1e+04;
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Best Local Similarity 93.8%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 1;
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GGAGGGGGAGGAGGG 17
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Best Local Similarity 88.9
Matches 16; Conservative
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; ORGANISM: Homo sapiens
PCT-US02-38216-18159
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Sequence 26652, Application PC/TUS0238216
Sequence 26652, Application PC/TUS0238216
Sequence 26652, Application:
TITLE OF INVENTION:
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
SOFTWARE: Patentin version 3.2
SEQ ID NO 26652
LENGTH: 19
                                                                                                                        RESULT 11
PCT-US02-38216-6220/c
; Sequence 6220, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6220
; LENGTH: 17
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PCT-US02-38216-38954
; Sequence 38954, Application PC/TUS0238216
; Sequence 38954, Application PC/TUS0238216
; GENERAL INFORMATION:
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.2
; SOFTWARE: Patentin version 3.2
; SOFTWARE: Patentin version 3.2
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Pred. No. 2.1e+04;
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Best Local Similarity 100.0%; P)
Matches 14; Conservative 0;
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Matches 14; Conservative 0;
        3 GGAGGGGGAGGAGGGG 18
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; ORGANISM: Homo sapiens
PCT-US02-38216-38954
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PCT-US02-38216-6220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 38912, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; TITLE OF INVENTION UMBER: PCT/US02/38216
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SEQ ID NO 38912
; SEQ ID NO 38912
; LENGTH: 19
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PCT-US03-11936A-126/c
; Sequence 126, Application PC/TUS0311936A
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION:
; FILE REFERENCE: 1551.2001003
; CURRENT APPLICATION NUMBER: PCT/US03/11936A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 21
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                                                                                                                                                                                                                                                                                                 Query Match 80.0%; Score 14.4; DB 1; Length 18; Best Local Similarity 93.8%; Pred. No. 1.5e+04; Matches 15; Conservative 0; Mismatches 1; Indels
        GENES AND USES THEREOF
TITLE OF INVENTION: GENES AND USES THEREOFFILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 41647
LENGTH: 18
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Best Local Similarity 93.89
Matches 15, Conservative
                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-41647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-38912
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Sequence 14763, Application PC/TUS0238216
Sequence 14763, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT PPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 14763
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ROSELTA GENOMICS LTD
APPLICANT: ROSELTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.2
SEQ ID NO 18314
LENGTH: 17
TYPE: DNA
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                                                                                        Query Match 77.8%; Score 14; DB 1; Length 19; Best Local Similarity 100.0%; Pred. No. 2e+04; Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                        RESULT 14
PCT-US02-38216-18314
; Sequence 18314, Application PC/TUS0238216
; GENERAL INFORMATION:
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CORGANISM: Homo sapiens
PCT-US02-38216-14763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
PCT-US02-38216-18314
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-26652
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PCT-US02-38216-14763
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AZ579189 1M0363112 AZ7560597 1M0554N21 AZ775540 2M0008H15 AZ783420 2M0025D07 AZ612326 1M0357118 AZ659755 1M0537F22 AZ772707 1M0583L18 AZ853126 2M0242012 AZ772707 1M0583L18 AZ853126 2M0242012 AZ853126 1M0056G10 AZ853126 1M0056G10 AZ8731988 1M0050B11 AZ871408 1M0050B11 AZ871408 2M0184B13 AZ647348 1M0520117 AZ871408 2M0184B13 AZ645874 1M0511C07 AZ871408 2M0184E16 AA918795 0169C05.5 AA96614 0526002xj AZ87199 1M0146P20 AZ87199 1M0146P20 AZ87199 1M0146P20 AZ87199 1M0146P20 AZ66896 1M0549A24 AZ87199 1M0146P20 AZ66896 1M0549A24 AZ66896 1M0549A24

AZ345792 AZ549189 AZ740597 AZ7750597 AZ78512326 AZ645269 AZ645269 AZ69597269 AZ6969440 AZ8712106 AZ8712106 AZ8712108 AZ883126 AZ883126 AZ883126 AZ8819030 AZ8819030 AZ8819030 AZ8819030 AZ8819030 AZ607348 AZ607348 AZ607348 AZ607348 AZ607348

us-09-331-204a-7.szlm22.rst

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 19)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished

Contact: Robert Strausberg, Ph.D.
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Trace considered overall poor qu
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. 19
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AI251781.1 GI:3848310
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Homo sapiens
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AZ876923 2M0192D07
AU254493 AU254493
AI582080 ar96b07.x
                                                                                 Search time 1581.77 Seconds (without alignments) 276.576 Million cell updates/sec
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Compugen Ltd
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AU254493
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18
1 ttggaggggaaggaggg 18
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Gapop 10.0 , Gapext 1.0
GenCore
Copyright (c) 1993
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Maximum Match 100%
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19 bp mRNA linear EST 05-NOV-1998 NCI CGAP Brn35 Homo sapiens cDNA clone IMAGE:1978032 3' TR:\(\overline{Q}3994\overline{9}\) HYDROXYPROLINE-RICH PROTEIN: ; mRNA

source

FEATURES

ALIGNMENTS

AZ579495 1M0367C13 AI434548 ti49d05.x AI735392 at10e10.x BQ585098 E011826-0

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AI582080/c
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AU254493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ876923 21-FEB-2001 2M0192D07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0192D07 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                               Gaps
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Insert Length: 10000 Std Error: 0.00
Plate: 0192 row: D column: 07
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0192D07"
organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
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Fax: 801 585 7177
Email: ddunn@genet
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84112, USA
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was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AU254493 3'-directed mouse cDNA library Mus musculus cDNA clone BED0002246 3', mRNA sequence.
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Kato, K. and Matoba, R.
Generation of expressed sequence tags from mouse brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BBD0002246"
/tissue_type="brain"
/clone_lib="3'-directed mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 21
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Email: kkato@bs.aist-nara.ac.jp,
URL:http://love2.aist-nara.ac.jp/BED/index.html.
Location/Qualifiers
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Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
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Best Local Similarity 93.3-
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

ACCESSION

TITLE JOURNAL COMMENT

FEATURES

DEFINITION

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1. i6
| organism="Homo sapiens"
| mol type="mRNA"
| db xref="taxon:9606"
| clone="IMAGE:1601157"
| tissue_type="pooled germ cell tumors"
| tissue_type="pooled germ cell tumors"
| lab host="DH10B"
| clone lib="NCI_CGAP_GC3"
| note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was

constructed by Bento Soares and M. Fatima Bonaldo. "
2 a 1 c 13 g 0 t
                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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19 bp DNA linear GSS 29-SEP-2000
1M0080G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0080G12 R, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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    1 (bases 1 to 16)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.2%; Score 13; DB 9; Length 16; 100.0%; Pred. No. 8.5e+05; ive 0; Mismatches 0; Indels
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
                                                                                                                                                                                                                                                                                                                                                                                                                Trace considered overall poor quality Insert Length: 514 Std Error: 0.00 Seg primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
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Mus musculus
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100.0%; Pre-
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                                                                                 Tumor Gene Index
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IMAGE:2173429 3' similar to SW:FOR4 MOUSE Q05859 FORMIN 4 ;contains
element MSR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 22)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 6.3e+05;
); Mismatches 2; Indels
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2173429"
/sex="male"
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AA968729.1 GI:3143909
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Homo sapiens
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BASE COUNT ORIGIN

RESULT 5 AA968729 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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E., SLC,

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Rm. 308, Biomedical Polymers Research Bldg., 20
                   B4112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0244 row: H column: 23
Seg primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0244H23"
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University of Utah Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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19 bp DNA linear GSS 04-OCT-2000 IM0244H23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0244H23 F, genomic survey sequence.
A2447248
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
Mouse whole genome scaffolding with paired end reads from 10kb
Unpublished
                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080G12"
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University of Utah Genome Center
University of Utah
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               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus suscendiata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                            Laboratory Mouse DNA Resource
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0554 row: N column: 21
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GGAGGGGAGGAGGGG 18
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                                                                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male"
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/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1M0554N21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0554N21 F, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                      20 S. 2030 E., SLC,
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0363 row: I column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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Contact: Robert B. Weiss
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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Best Local Similarity 87.5%; Pred. No. 9.7e+05;
Matches 14; Conservative 0; Mismatches 2;
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ΤD

COMMENT

FEATURES

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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA_polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                      Contact: Robert B. Weiss University of Utah Genome Center University of Utah Genome Center University of Utah Genome Center BM: 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0025 row: D column: 07 Seq primer: CGTTGTAAAACGACGCCAGT
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71.1%; Score 12.8; DB 28; Length 19;
Best Local Similarity 87.5%; Pred. No. 9.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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Location/Qualifiers
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AZ512326/c
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Laboratory Mouse DNA Resource
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was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored bNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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2M0025D07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0025D07 F, genomic survey sequence.
AZ783420
AZ783420.1 GI:12918130
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0008 row: H column: 15
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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| /organism="Mus musculus"
| /mol_type="genomic DNA"
| strain="C57BL/6J"
| /db_xref="taxon:10090"
| /clone="UUGC2M0008H15"
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Matches 14; Conservative
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AZ512326
1M0357118R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0357118 R, genomic survey sequence.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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ACCESSION

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REFERENCE AUTHORS

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Mouse whole genome scaffolding with paired end reads from 10kb
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Mus musculus
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87.5%;
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Matches 14; Conservative
                                plasmid inserts
Unpublished
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1M0510B10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0510B10 R, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E.,
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                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0357 row: I column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
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/clone="UUGC1M0357118"
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Matches 14, Conservative
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/sex="Mouse Documents of the control of the control
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1M0537F22F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0537F22 F, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0510 row: B column: 10
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/clone="UUGCIM0510B10"
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                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
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musculus_C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse_DNA_Resource
                       Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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and Wright, D., Weiss, R.
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwb42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
"" 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0583 row: L column: 18
Seg primer: CACACAGGAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CS7BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="UUGC1M0583L18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 20.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GGAGGGGAGGAGGGG 18
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Best Local Simi
Matches 14;
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Sequence 282, App
Sequence 53, Appl
Sequence 59, Appl
Sequence 64, Appl
Sequence 64, Appl
Sequence 83, Appl
Sequence 83, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Appli
Sequence 44, Appl
Sequence 4, Appli
Sequence 45, Appl
Sequence 127, App
Sequence 93, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 30, Appl
Sequence 26, Appl
Sequence 9, Appli
                                                                                                             // Search time 41.3143 Seconds
(without alignments)
192.304 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 59, Sequence 59, Sequence 64, Sequence 64, Sequence 64, Sequence 59, Sequence 57, Beguence 51, Begue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 45,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
5.1.6
Compugen Ltd.
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US-08-529-878B-3
US-08-529-878B-44
US-08-529-878B-44
US-08-529-878B-45
US-09-780-1127
US-09-780-1127
US-09-780-1127
US-09-495-140-26
US-09-495-140-26
US-09-496-1753-30
US-09-496-1753-30
US-09-496-1753-53
US-09-496-1753-64
US-08-863-639A-53
US-08-863-6339A-53
US-08-863-6339A-53
US-08-863-6339A-53
US-08-388-613A-51
US-08-398-611A-51
US-08-398-611A-51
US-08-398-611A-51
US-08-398-611A-51
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 version 9
- 2003 (
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
 GenCore (c) 1993
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18
1 ttggagggggaggag
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                   Copyright
                                                                                                                                                                                                                                                                                                                                                                                                              length: 0
length: 22
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Match
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                                                                                                                                                                                           Title:
Perfect
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Maximum |
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Type,
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Diagnosis
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APPLICANT: Moncany, Maurice
APPLICANT: Montagnier, Luc
TITLE OF INVENTION: Nucleotide Sequences Derived From The
TITLE OF INVENTION: Genome Of Retroviruses Of The HIV-1, HIV-2 And SIV 1
TITLE OF INVENTION: Genomes Of These Retroviruses And For The In Vitro I
TITLE OF INVENTION: Of The Diseases Due To Those Viruses
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
   Appl
Appl
Appl
Appl
Appl
Appl
                             Sequence 38, A Sequence 38, A Sequence 38, A Sequence 38, A Sequence 2, Ap Sequence 2, Ap
                                                                                                                                              Sequence 3
  Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,077
FILING DATE:
US-08-491-334A-51
US-08-491-334A-51
US-08-491-334A-54
US-09-027-449-38
US-09-027-449-38
US-09-121-952A-38
US-09-234-368-38
US-09-234-368-38
US-08-486-913-2
US-08-486-913-2
US-08-486-535-2
US-08-486-535-3
US-08-486-535-3
US-08-486-535-3
                                                                                                                                                                                                                                                                                                                                                    STREET: 1300 I Street, N.W., Suite 700 CITY: Washington STATE: D.C. COUNTRY: Usb
                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/472,928
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/160,465
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 8912371
FILING DATE: 20-SEP-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                             Sequence 45, Application US/09092077
Patent No. 6194142
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FR 8907354
FILING DATE: 06-FEB-1989
ATTORNEY/AGENT INFORMATION:
               RESULT 1
US-09-092-077-45
   444444444400000000000
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REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0062-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000

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(202)408-4400

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

```
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Crockett & Fish STREET: 3000 S. Augusta Court CITY: La Habra STREET: 4000 S. Augusta Court CITY: La Habra STATE: California COUNTRY: United States of America STATE: California COUNTRY: United States of America STATE: P0631
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/529,878B FILING DATE: 13-SEP-1995
CLASSIFICATION NUMBER: 33,880
REGISTRATION NUMBER: 33,880
REFERENCE/DOCKET NUMBER: 213/003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 714-525-3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tam, Robert C.

APPLICANT: Tam, Robert C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: Crockett & Fish

STREET: 3000 S. Augusta Court

CITY: La Habra

STATE: California

COUNTRY: United States of America

ZIATE: DANSER COURT

ZIATE: DANSER COURT

ZIATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.2%; Score 14.8; DB 2;
88.9%; Pred. No. 8.2e+02;
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COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/529,878B

FILING DATE: 13-SEP-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Fish, Robert D.

REGISTRATION NUMBER: 33,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-529-878B-4
; Sequence 4, Application US/08529878B
; Patent No. 5932556
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 16; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-529-878B-44
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O
                                                                                                                                                                                                                             Query Match 85.6%; Score 15.4; DB 3; Length 21; Best Local Similarity 94.1%; Pred. No. 4.8e+02; Matches 16; Conservative 0; Mismatches 1; Indels
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US-08-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 44, Application US/08529878B
Patent No. 5932556
GENERAL INFORMATION:
APPLICANT: Tam, Robert C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TTGGAGGGGGAGGGGG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                      3 TGGAGGGGGAGGAG 19
                                         ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLGGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-092-077-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
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SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
EDNESS: unknown
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             21 base pairs
                                       nucleic acid
EDNESS: single
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US-08-529-878B-3
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Length 18 Indels

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                   RESULT 6
US-08-173-489C-127/c
; Sequence 127, Application US/08173489C
; Patent No. 586124
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
APPLICANT: WANG, C. -G.
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
; STREET: NEW YORK
; STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The 3' untranslated regions of the duplicated human alpha-globin genes are unexpectedly divergent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DATE: 1980
RELEVANT RESIDUES IN SEQ ID NO: 127 :FROM 1 TO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: alpha-1-globin gene (accession
DESCRIPTION: V00491) nucleotides 827 to 843
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Michelson, A M, Orkin, S H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ,00-188
(212) 246-8959
127:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 GGAAGGGGAGGAGGG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (attorney) (21 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 15; Conserv
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US-09-780-173A-93
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                                                                                                                                                                                                                                                                                                         Length 21;
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Sequence No. 593256

Fatent No. 593256

GENERAL INFORMATION:
APPLICANT: Tam, Robert C.
TITLE OF INVENTION: RETHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
NUMBER OF SEQUENCE: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Crockett & Fish
STREET: 3000 S. Augusta Court
CITY: La Habre
STREET: California
CCUNTRY: United States of America
STATE: California
CCUNTRY: United States of America
STATE: California
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordFrefect 6.1
APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fish, Robert D.
REGISTRATION NUMBER: 213/003
TELEPHONE: 714-525-3303
TELEPHONE: 714-525-3303
                                                                                                                                                                                                                                                                                                    Query Match 82.2%; Score 14.8; DB 2; Best Local Similarity 88.9%; Pred. No. 8.2e+02; Matches 16; Conservative 0; Mismatches 2;
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REFERENCE/DOCKET NUMBER: 2:
TELECOMMUNICATION INFORMATION
TELEPHONE: 714-525-3433
TELEFAX: 714-525-3303
                                                                                                                                                                                                                ; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-529-878B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.2%;
88.9%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
                                                          TELEFAX: 714-525-3303
TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.9
Matches 16; Conservative
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US-08-529-878B-45
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) OTHER INFORMATION: Description of Artificial Sequence:/No. 6376182e = / QTHER INFORMATION: Synthetic construct US-09-495-140-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Brenda F. Baker
APPLICANT: Brenda F. Baker
APPLICANT: Lex M. Cowsert
TITLE CANTINENSE MODULATION OF ETS-2 EXPRESSION
FILE REFERENCE: RTS-0063
CURRENT APPLICATION NUMBER: US/09/344,579
CURRENT FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 9
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                    Length 17;
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APPLICANT: Lex M. Cowsert
TITLE CANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
FILE REFERENCE: RTS-0120
CURRENT APPLICATION NUMBER: US/09/490,692
CURRENT FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 176
SEQ ID NO 153
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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CTHER INFORMATION: Antisense Oligonucleotide
US-09-490-692-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , OTHER INFORMATION: Antisense Oligonucleotide US-09-344-579-9
                         EARLIER FILING DATE: 1999-09-03
EARLIER APPLICATION NUMBER: 08/856,141
EARLIER FILING DATE: 1997-05-14
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 153, Application US/09490692; Patent No. 6180353; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/09344579 Patent No. 6054316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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US-09-490-692-153/c
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US-09-344-579-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                                            GENERAL INFORMATION:
APPLICANT: Robert McKay
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA PRIME EXPRESSION
FILE REFERENCE: RTS-0165
CURRENT PPLICATION UNMBER: US/09/780,173A
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 95
SEQ ID NO 93
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CHAO, LEE
APPLICANT: CHAO, JULIE
APPLICANT: CHAO, JULIE
APPLICANT: CHAO, JULIE
APPLICANT: CHAO, JULIE
APPLICANT: CONG, QING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING
TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH TREATMENT
TITLE OF INVENTION: OF ESSENTIAL HYPERTENSION
FILE REFERENCE: 19113.0081
CURRENT APPLICATION NUMBER: US/09/495,140
CURRENT FILING DATE: 2000-01-31
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TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA FILE REFERENCE: ISPH-0498
CURRENT APPLICATION NUMBER: US/09/661,753
CURRENT FILING DATE: 2000-09-14
EARLIER APPLICATION NUMBER: 60/154,546
EARLIER FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 68
SEQ ID NO 30
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.7%; Score 13.8; DB 4; Length 20; 88.2%; Pred. No. 2e+03; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.4%; Score 13.4; DB 4; Length 20; 93.3%; Pred. No. 2.8e+03; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Antisense Oligonucleotide US-09-780-173A-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Antisense Oligonucleotide US-09-661-753-30
Application US/09780173A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-495-140-26; Sequence 26, Application US/09495140; Patent No. 6376182; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-661-753-30/c; Sequence 30, Application US/09661753; Patent No. 6436909; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGAGGGGAGGAGGGG 18
                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 15; Conserv
  Sequence 93,
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                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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APPLICANT: Prockop, Darwin J.
APPLICANT: Ala-Kokko, Leena
APPLICANT: Ala-Kokko, Leena
APPLICANT: Williams, Charlene J.
APPLICANT: Williams, Clinton
APPLICANT: Baldwin, Clinton
APPLICANT: Ahmad, Nilofer Nina
TITLE OF INVENTION: Methods of Detecting A Genetic
NUMBER OF SEQUENCES: 293
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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Query Match 71.1%; Score 12.8; DB 3; Length 20; Best Local Similarity 87.5%; Pred. No. 4.7e+03; Matches 14; Conservative 0; Mismatches 2; Indels
                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRI: COLD
COUNTRI: COLD
COMPUTER: 19103
COMPUTER: DISKETTE, 3.5 INCH
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,426B
FILING DATE: 03-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION 0ATA:
APPLICATION NUMBER: PCT/US93/10964
FILING DATE: 12-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,284
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: MARK DELUCA
REFERENCE/DOCKET NUMBER: TJU-1082
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 282:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                            US-08-256-426B-282/c; Sequence 282, Application US/08256426B; Patent No. 5948611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-08-863-639A-41
; Sequence 41, Application US/08863639A
; Patent No. 5981185
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71.1%; SC
Best Local Similarity 87.5%; Pr
Matches 14; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: I
US-08-256-426B-282
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ARREAL INFORMATION:
AREAL MARGONING TO ARE S.
ARPLICANT MARGON, ROBER S.
ARPLICANT MARGONING S.
AREAL S.
AREAL MARGONING S.
ARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP 91101
COMPUTER: Lab Compatible
CORPUTER: IBM Compatible
CORPUTER: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
CORPUTER: IBM Compatible
CORPUTER: Tem Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURSSIT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
CLASSIFICATION WHERE: 20,532
ATTORNEY/AGENT INFORMATION:
NAME: JOSEPH E. Mueth
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 20,532
REFERENCE CHARACTERISTICS:
LENGTH: 31 base pairs
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: Other nucleic acid
US-08-863-639A-59

71.1%; Score 12.8; DB 2; Left
CONTRACTION TYPE: Other nucleic acid
US-08-863-639A-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Cassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TILLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                     TELEFAX: (626) 795-9321
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-863-639A-59/c
; Sequence 59, Application US/08863639A
; Patent No. 5981185
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Joseph E. Mueth
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 1185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GGAGGGGGAGGAGGGG 18
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Search completed: October 27, 2003, 14:03:35 Job time : 42.3143 secs

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October 27, 2003, 11:25:34 ; Search time 387.943 Seconds (without alignments) 124.432 Million cell updates/sec
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: cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

: cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

: cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

: cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

: cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

: cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

: cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

: cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

: cgn2_6/ptodata/1/pubpna/USO96_PUBCOMB.seq:*

: cgn2_6/ptodata/1/pubpna/USO06_PUBCOMB.seq:*

: cgn2_6/ptodata/1/pubpna/USO06_NEW_PUB.seq:*

: cgn2_6/ptodata/1/pubpna/USO06_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 1934, Ap				. რ		30,		47	899	Sequence 900, App	901,	1932,	Sequence 1938, Ap	5	α
SUMMARIES		QH	US-10-061-201-1934	US-10-061-201-1935	US-10-061-201-1936	US-09-828-034-28	US-10-061-201-1933	US-10-061-201-1937	US-09-948-002-30	US-09-780-533A-46	US-09-780-533A-47	US-09-780-533A-899	US-09-780-533A-900	US-09-780-533A-901	US-10-061-201-1932	US-10-061-201-1938	US-09-780-533A-45	US-09-780-533A-894
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US-10-059-877-2	US-10-303-10	US-10-059-888-2	US-09-919-501-1	US-10-032-585-40	US-10-181-846	09-828-034-9	US-10-258-860-1	US-09-726-258-3	US-09-780-533A-9	US-09-930-423-86	US-09-745-237A-86	US-10-060-756A-6	39-854-883-174	US-09-780-533A-89	US-10-061-201-193	US-10-061-201-19	US-10-314-405-4	US-10-059-877-2	US-10-339-161-2	US-10-059-888-22	US-09-780-533A-8	US-09-780-533A-89	US-09-740-332-183	US-09-817-879-183	US-09-940-244-16	US-09-864-636A-2	US-10-290-38	US-10-084-839-21
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ALIGNMENTS

Sequence 1934, Application US/10061201
; Sequence 1934, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION: Mark
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/328,205
PRIOR APPLICATION NUMBER: US 60/328,205 SOFTWARE: Aeomica Sequence Listing Engine SEQ ID NO 1934 LENGTH: 17 ORGANISM: Homo sapiens US-10-061-201-1934

DB 12; Length 17; 83.3%; Score 15;

Query Match

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Gaps
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ORGANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-28
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88.9%; Pred. No. 6e+03;
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83.3%; Score 15; DB 12; I
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 28, Application US/09828034
) Patent No. US20020064771A1
GENERAL INFORMATION:
APPLICANT: Zhong, Weidong
APPLICANT: Hong, Zhi
APPLICANT: Hong, Zhi
APPLICANT: Hong, Zhi
FILE REFERENCE: IN01165
CURRENT APPLICATION NUMBER: US/09/828,034
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: U.S. 60/195,852
PRIOR PILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 28
LENGTH: 21
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; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFRENCE: P80178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
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                                        PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: DO 09/864,761
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-05-23
PRIOR FILING DATE: 2001-01-0
NUMBER OF SEQ ID NOS: 4162
SEQ ID NO 1936
LENGTH: 17
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Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1936
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US-10-061-201-1933/c
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                                           Indels
Best Local Similarity 100.0%; Pred. No. 5.3e+03; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                Sequence 1935, Application US/10061201
Publication No. US20030166229A1
GENERAL INFORMATION:
APPLICANT: Shannon, Mark
TILLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PB0178
CURRENT FILING DATE: 2002-01-30
PRIOR PELICATION NUMBER: PCT/US01/00666
PRIOR PELICATION NUMBER: PCT/US01/00667
PRIOR PELICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/00668
PRIOR PELICATION NUMBER: PCT/US01/00669
PRIOR PELING DATE: 2001-01-30
PRIOR DATE: 2001
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Sequence 1936, Application US/10061201

Publication No. US20030166229A1

GENERAL INFORMATION:

APPLICANT: Shannon, Mark

TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1

FILE REFERENCE: PB0178

CURRENT FILING DATE: 2002-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                         RESULT 2
US-10-061-201-1935/c
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RESULT 8

US-09-780-533A-46/c

i Gequence 46, Application US/09780533A

publication No. US2030060611A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Hacberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBHB00,878-A (400/011)
CURRENT APPLICANTION UNMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: PatentIn version 3.0

SEQ ID NO 46

FILE REFERENCE: MCS A CONTACT OF THE CALL OF THE
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US-09-948-002-30/c
IS-09-948-002-30/c
Sequence 30, Application US/09948002
Publication No. US20030050265A1
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: Susan F. Murray
TITLE OF INVENTION: FACTOR BETA EXPRESSION
FILE REFERENCE: ISPH-0607
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 09/661,753
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 30
LENGTH: 20
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                                                                     Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 74.4%; Score 13.4; DB 11; Best Local Similarity 93.3%; Pred. No. 2e+04; Matches 14; Conservative 0; Mismatches 1;
                                                                                                          1.3e+04;
                                                              Score 14; DB 12;
Pred. No. 1.3e+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Antisense Oligonucleotide US-09-948-002-30
                                                              Query Match

Best Local Similarity 100.0%; P
Matches 14; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GGAGGGGGAGGAGGG 17
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; ORGANISM: Homo sapiens
US-09-780-533A-46
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Publication No. US20030166229A1

GENERAL INFORMATION:

APPLICANT: Shannon, Mark

TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PB0178

CURRENT APPLICATION NUMBER: US/10/061,201

CURRENT FILING DATE: 2002-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-05-23
PRIOR PRILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 4162
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 1933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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17.8%; Score 14;
Best Local Similarity 100.0%; Pred. No.
Matches 14; Conservative 0; Mismatch
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SEQ ID NO 1937
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; ORGANISM: Homo sapiens
US-10-061-201-1937
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RESULT 12
US-09-780-533A-901/c

Sequence 901, Application US/09780533A

Publication No. US20030060611A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Haeberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBHB00, 878-A (400/011)
CURRENT FILING DATE: 2001-02-09
FRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: Patentin version 3.0
SEQ ID NO 901
                                      APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Chowrira, Bharat
APPLICANT: Haeberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBHB00,878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT APPLICATION NUMBER: US 60/181,797
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: Patentin version 3.0
SEQ ID NO 900
LENGTH: 17
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Publication No. US20030166229A1
GENERAL INFORMATION:
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PB0178
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT FILING DATE: 2002-01-30
      Publication No. US20030060611A1
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Best Local Similarity 100.
Matches 13; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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TYPE: RNA
CNGANISM: Homo sapiens
US-09-780-533A-901
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ORGANISM: Homo sapiens
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US-09-780-533A-47/c

Sequence 47, Application US/09780533A

Publication No. US20030060611A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Blatt, Larry

APPLICANT: Chowrira, Bharat

APPLICANT: Haeberli, Pete

TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene

FILE REFERENCE: MBHB00,878-A (400/011)

CURRENT FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: US 60/181,797

PRIOR APPLICATION NUMBER: US 60/181,797

NUMBER OF SEQ ID NOS: 6679

SOFTWARE: Patentin version 3.0

LENGTH: 17

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LENGTH: 17

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Publication No. US20030060611A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Brart
APPLICANT: Chowrita, Bharat
APPLICANT: Haeberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBHB00, 878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
NUMBER OF SEQ ID NOS: 6679
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Pred. No. 3e+04;
0; Mismatches 0; Indels
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US-09-780-533A-900/c
; Sequence 900, Application US/09780533A
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Best Local Similarity 100.0%; P:
Matches 13; Conservative 0;
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TYPE: RNA
CORGANISM: Homo sapiens
US-09-780-533A-899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-47
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US-09-780-533A-899/c
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Gaps

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Sequence 45 Application US/09780533A

Publication No. US20030060611A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Blatt, Larry

APPLICANT: Haeberli, Pete

TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene

FILE REFERENCE: MBHB00,878-A (400/011)

CURRENT APPLICATION NUMBER: US/09/780,533A

CURRENT FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: US 60/181,797

SOFTWARE: Patentin version 3.0

SEQ ID NO 45

LENGTH: 17
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                                                                                 72.2%; Score 13; DB 100.0%; Pred. No. 3ettive 0; Mismatches
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                                                                                    Query Match
Best Local Similarity 100.
Matches 13; Conservative
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CRGANISM: Homo sapiens
US-09-780-533A-45
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                     US-10-061-201-1938
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Publication No. US20030166229A1

GENERAL INFORMATION:
APPLICANT: Shannon, Mark
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: P80178
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT APPLICATION NUMBER: US/10/0666
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/864, 761
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 4162
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 1932
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SEQ ID NO 1938
LENGTH: 17
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; ORGANISM: Homo sapiens
US-10-061-201-1932
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US-10-061-201-1938/c
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cgn2_6/ptodata/1/pna/PCTUS_COMB.seq:*

cgn2_6/ptodata/1/pna/US06_COMB.seq:*

cgn2_6/ptodata/1/pna/US08_COMB.seq:*

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cgn2_6/ptodata/1/pna/US086_COMB.seq:*

cgn2_6/ptodata/1/pna/US086_COMB.seq:*

cgn2_6/ptodata/1/pna/US081_COMB.seq:*

cgn2_6/ptodata/1/pna/US081_COMB.seq:*
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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Maximum DB s
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/pna/v3101B_COMB.seq:*
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//pna/v3103B_COMB.seq:*
/pna/v3103B_COMB.seq:*
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1/pna/US6019 COMB.seq:*
1/pna/US6020 COMB.seq:*
1/pna/US6021 COMB.seq:*
1/pna/US6022 COMB.seq:*
1/pna/US6023A COMB.seq:*
1/pna/US6023A COMB.seq:*
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COMB.seq:*
COMB.seq:*
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'pna/US104B_COMB.seq:'
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/pna/US6011_c
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/pna/US6002
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ptodata/1/pna/US6016
ptodata/1/pna/US6017
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% Query Match Length DB	DB	ΠD	Description
, -	1	100.0		9	US-09-331-	Sequence 7, Appli
2	18	100.0		19	US-09-331-204-4	Sequence 4, Appli
m	17	94.4		50	19 50 US-10-310-188-47426	Sequence 47426, p
4	16.4	16.4 91.1		19	US-09-331-204-5	Sequence 5. Appli

0 0 0 0 0 0 0

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Sequence 47426, Application US/10310188

Sequence 47426, Application US/10310188

GENERAL INFORMATION:
APPLICANT: ROSELtaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEI
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT PILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 47426
LENGTH: 19
                                                    Sequence 4, Application US/09331204
; Sequence 4, Application US/09331204
; GENERAL INFORMATION:
    APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN TITLE OF INVENTION: IMMUNE RESPONSE
; FILE REFERENCE: ICNSequence
; CURRENT APPLICATION NUMBER: US/09/331,204
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver: 2.0
; SEQ ID NO 4
; LENGTH: 19
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OTHER INFORMATION: Description of Artificial Sequence: An oligomer
OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
OTHER INFORMATION: acid. This term includes oligomers consisting of
OTHER INFORMATION: naturally occurring bases, sugars and intersugar (US-09-331-204-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-09-331-204-5
; Sequence 5, Application US/09331204
; GENERAL INFORMATION:
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING;
; TITLE OF INVENTION: IMMUNE RESPONSE
; FILE REFERENCE: ICNSequence
; CURRENT APPLICATION NUMBER: US/09/331,204
; CURRENT FILING DATE: 1999-08-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 18; DB 19; Best Local Similarity 100.0%; Pred. No. 7.1e+03; Matches 18; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                              LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-47426
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General INFORMATION:
GENERAL INFORMATION:
APPLICANT: Itam, Robert
TITLE OF INVENTION:
G-rich Oligo Aptamers and Methods of Modulating an Immune Response Title OF INVENTION NUMBER: US/09/331,204A
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: OF/US97/23927
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
Sequence 45, Appli
Sequence 45, Appl
Sequence 1934, Ap
Sequence 1936, Ap
Sequence 17, Appli
Sequence 47, Appli
Sequence 47, Appli
Sequence 28, Appli
Sequence 18159, A
Sequence 1913, A
Sequence 39031, A
Sequence 1933, Ap
Sequence 1933, Ap
Sequence 1933, Ap
Sequence 1933, Ap
Sequence 2655, Ap
Sequence 1933, Ap
Sequence 26652, Ap
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                US-08-472-928B-45
US-09-670-105-45
US-10-061-201-1934
US-10-061-201-1934
US-10-061-201-1934
US-60-328-205-1936
US-60-328-205-1936
US-08-387-041A-3
US-08-387-041A-4
US-08-381-204-1
US-08-381-204-6
US-08-381-204A-6
US-10-310-188-389312
US-10-310-188-389312
US-10-310-188-38932
US-10-310-188-38932
US-10-310-188-38932
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Matches 18; Conserv
 US-09-331-204A-7
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APPLICANT: Moncany, Maurice
APPLICANT: Montagnier, Luc
Montagnier, Luc
TITLE OF INVENTION: Nucleotide Sequences Derived From The
Genome Of Retroviruses Of The HIV-1, HIV-2 And SIV Type,
And Their Uses In Particular For The Amplification Of The
Genomes Of These Retroviruses And For The In Vitro Diagnor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/670,105
FILING DATE: 26-Sep-2000
CLASSIFICATION: <UNKNOWn>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                        MEDIUM TYPE: Floppy dish.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,928B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160,465
FILING DATE: 02-DEC-1993
PRIOR APPLICATION MUMBER: PR 8912371
FILING DATE: 20-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PR 8907354
FILING DATE: 06-FEB-1989
PRIOR APPLICATION NUMBER: 25,146
FILING DATE: 06-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REFERENCE/DOCKET NUMBER: 02356.0062-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4400
TELEPHONE: (202)408-4400
TELEFAX: Closh408-4400
TELEFAX: CLOSH408-4400
TELEFAX: CLOSH408-4400
TELEFAX: CLOSH408-4400
TELEFAX: LENGTH: 21 base pairs
TYPE: nucleic acid
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Pred. No. 6.4e+04;
0; Mismatches 1;
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APPLICATION NUMBER: 09/092,077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-670-105-45; Sequence 45, Application US/09670105; GENERAL INFORMATION:
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Best Local Similarity 94.1%;
Matches 16; Conservative (
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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GENERAL INFORMATION:
APPLICANT: ICN Pharmaceuticals, Inc.
APPLICANT: Tam, Robert
TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Respondence 216/013-US1
CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/VS97/23927
PRIOR APPLICATION NUMBER: PCT/VS97/23927
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Moncany, Maurice
APPLICANT: Montagnier, Luc
APPLICANT: Montagnier, Luc
APPLICANT: Montagnier, Luc
TITLE OF INVENTION: Muleotide Sequences Derived From The
TITLE OF INVENTION: And Their Uses Of The HIV-1, HIV-2 And SIV Type,
TITLE OF INVENTION: Genome of Fatroviruses And For The Amplification Of The
TITLE OF INVENTION: Of The Diseases Due To Those Viruses
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: An oligomer OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic OTHER INFORMATION: acid. This term includes oligomer's consisting of OTHER INFORMATION: naturally occurring bases, sugars and intersugar (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 2.7e+04;
0; Mismatches 1;
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Pred. No. 2.7e+04;
O. Mismatches 1;
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CITY: Washington
    PCT/US97/23927
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
LENGTH: 18
Type
PRIOR APPLICATION NUMBER: PCT
PRIOR FILING DATE: 1997-12-19
                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: synthetic construct US-09-331-204A-8
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Best Local Similarity 94.4%;
Matches 17; Conservative
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                                                                          Indels
                                      Best Local Similarity 100.0%; Pred. No. 8.9e+04; Matches 15; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                             RESULT 9

US-10-061-201-1935/C

Sequence 1935, Application US/10061201

GENERAL INFORMATION:

APPLECANT: Shannon, Mark

TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1

FILE REFERENCE: PB0178

CURRENT APPLICATION NUMBER: US/10/061,201

CURRENT FILING DATE: 2002-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR PRIOR FILING DATE: 2001-01-30

PRIOR PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2
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APPLICANT: Shannon, HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PB0178
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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                                                                                                                                            4 GAGGGGGAGGAGGGG 18
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; ORGANISM: Homo sapiens
US-10-061-201-1935
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FILING DATE: <UNKnown>
APPLICATION NUMBER: US/08/472,928
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/160,465
FILING DATE: 02-DE2-1993
APPLICATION NUMBER: FR 8912371
FILING DATE: 20-SEP-1989
APPLICATION NUMBER: FR 8907354
FILING DATE: 06-FEB-1989
APTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0062-02000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
TELEPHONE: (202)408-4000
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Shannon, Mark
ITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PB0178
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT FILING DATE: 2002-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-05-23
PRIOR PILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-06-3
PRIOR FILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 4162
SOFTWARE: Abomica Sequence Listing Engine
SEQ ID NO 1934
LENGTH: 17
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MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-670-105-45
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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; ORGANISM: Homo sapiens
US-10-061-201-1934
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Best Local Similarity
Matches 16; Conserva
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RESULT 14
US-10-310-188-6227/c
; Sequence 6227, Application US/10310188
; GENERAL INFORMATION:
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Best Local Similarity 100.0%; P
Matches 15; Conservative 0;
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                               4 GAGGGGGAGGAGGGG 18
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Best Local Similarity 100.
Matches 15; Conservative
                                                                        16 GAGGGGGAGGAGGGG
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CORGANISM: Homo sapiens
US-60-328-205-1936
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                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1936
LENGTH: 17
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83.3%; Score 15; DB 87; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 0; Indels
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Pred. No. 8.9e+04;
0; Mismatches 0;
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y 100.0%; Pred, No. 8.9e+04;
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; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: AEOMICA-26
; CURRENT APPLICATION NUMBER: US/60/328,205
; CURRENT FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1935
; LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-60-328-205-1934/c
; Sequence 1934, Application US/60328205
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: ABOMICA-26
; CURRENT APPLICATION NUMBER: US/60/328,205
; CURRENT FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1934
; LENGTH: 17
PRIOR APPLICATION NUMBER: PCT/USO1/UU0000
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-3
PRIOR FILING DATE: 2001-05-3
PRIOR FILING DATE: 2001-05-3
PRIOR FILING DATE: 2001-010
NUMBER OF SEQ ID NOS: 4162
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 1936
LENGTH: 17
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Best Local Similarity 100.0%; Pr
Matches 15; Conservative 0;
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Best Local Similarity 100.0%; Pr
Matches 15; Conservative 0;
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; ORGANISM: Homo sapiens
US-60-328-205-1934
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CORGANISM: Homo sapiens
US-60-328-205-1935
                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1936
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US-60-328-205-1935/c
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APPLICANT: ROSELTAGEMONICS
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 6227
LENGTH: 18
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US-10-303-778-16894
; Sequence 16894, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: ROSELtaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
; TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16894
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Pred. No. 8.9e+04;
0; Mismatches 0;
RESULT 13
US-60-328-205-1936/c
; Sequence 1936, Application US/60328205
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: AEOMICA-26
; CURRENT APPLICATION NUMBER: US/60/328,205
; CURRENT FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
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Query Match 83.3%; Score 15; DB 50; Length 19; Best Local Similarity 100.0%; Pred. No. 8.9e+04; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-16894
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0; Gaps

Search completed: October 27, 2003, 17:52:53 Job time : 2356.29 secs

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Reduction; T cell; CD28; gene expression; treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; psoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2; systemic lupus erythematosus; inflammatory bowel disease; IL-2; production; antisense; inhibition; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD28 expression inhibiting oligonucleotide, RT05s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                 AAH50875
AAD03330
ABK00046
ABK00047
ABK00899
                                                                                                                                                                                                                                           ABK00900
ABK00901
ABV91219
ABV91225
AAV55680
AAF01954
                                            AAZ99625
AAZ99650
AAT36197
AAX90329
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AAA38350
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AAF16593
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95US-0529878.
95US-0387041.
95US-0529878.
96WO-US01507
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(first entry)
09-FEB-1995;
18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9624380-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
16-APR-1997
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AAT36242
000000000 00000
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                                                                                                                                                                                                                                                                                                                      N. Geneseq 19Jun03:*

| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
| SIDS1/gcgdata/geneseqn/emb1/NA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
| SIDS1/gcgdata/geneseqn/emb1/NA1984.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
                                                                         October 27, 2003, 10:32:29; Search time 162 Seconds (without alignments) 299.938 Million cell updates/sec
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                           2552756 seqs, 1349719017 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                       Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT36242
AAX90335
AAT36243
AAX90336
AAQ06932
AAT98040
ABV91221
ABV91222
                                                         nucleic search, using sw model
                                                                                                                                                                         IDENTITY NUC Gapoxt 1.0
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seg length: 22
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Score

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Scoring table:

Searched:

Human Ets-2 phosph 3' flanking sequen Human psoriasis-li Human psoriasis-li Feline immunodefic

Oestrogen receptor Human NOGO Hammerh Human NOGO Inozyme Human tissue kalli ö

us-09-331-204a-7.szlm22.rng

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18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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16-APR-1997
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                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                             AAT36243;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN).
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                 The present oligonucleotide reduces CD28 dependent interleukin-2 (IL-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated disease, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
immune system mediated disease; gamma-interferon; IL-8;
phosphorothioate; ss.
                                                         gene expression in T cells . e.g. graft vs. host disease,
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0
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                                                                                                                                                                                                                                                                Length 18;
                                                                                                                                                                                                                                                     100.0%; Score 18; DB 17; Length 18
100.0%; Pred. No. 5e+02;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      CD28 inhibiting phosphorothioate oligonucleotide RT05S.
                                                                                                                                                                                                                in cytokine release. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                           Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;
                                                                     for treating immune system diseases, septic shock, psoriasis, etc.
                                                           Oligo:nucleotide which reduces CD28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example, Column 24; 45pp; English.
                                                                                                   Example 2; Page 45; 77pp; English.
                                                                                                                                                                                                                                                                                                       TTGGAGGGGAGGGGG 18
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                                                                                                                                                                                                                                                                                                                                                                            AAX90335 standard; DNA; 18 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity Lovers
Thes 18; Conservative
(ICNC ) ICN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-443609/37
                                        WPI; 1996-384228/38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                AAX90335;
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                     Tam RC;
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AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothicate oligonuclectide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reduction; T cell; CD28; gene expression; treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; psoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2; systemic lupus erythematosus; inflammatory bowel disease; IL-2; production; antisense; inhibition; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present oligonucleotide reduces CD28 dependent interleukin-2 (1L-2) production and T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.

(Updated on 25-MAR-2003 to correct PR field.)
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                                                                                                                                                                                                                                                                                                                                                         ·.
                                                                                                                                                                                                                                                                                      Length 18;
                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                100.0%; Score 18; DB 20; 100.0%; Pred. No. 5e+02;
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                                                                                                                                                                                                                Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                              1 TTGGAGGGGAGGAGGGG 18
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95US-0529878.
95US-0387041.
95US-0529878.
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(first entry)
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                 present invention.
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AAX90336

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amplification; gag; vpr; pol; vpu; HIV-1; HIV-2; SIV; nef2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This nucleotide sequence is found in posn. 6228-6208 of HIV-2 ROD and 6141-6121 of SIV-MAC. It is the anti-sense strand of a primer pair used to amplify these HIV-1, HIV-2 and SIV viral sequences, esp. in conjunction with in vitro diagnosis of infection. It is useful for treating viral diseases, eg. AIDS. See also AAQ06905-31 and AAQ06933-54. (Updated on 09-JAN-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                               New nucleotide sequences derived from genome of HIV-1, HIV-2 and SIV - useful as primers for amplification of immuno-deficiency viruses in diagnosis and for raising antibodies in treatment of HIV infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human or simian immunodeficiency virus detection primer MMy24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
      MMy24 nucleotide constituent of vpx gene of HIV-2 ROD and SIV-MAC.
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Pred. No. 4.5e+03;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21 BP; 5 A; 2 C; 13 G; 1 T; 0 other;
                                                         HIV-2; SIV; AIDS; anti-sense nucleotide;
                                                                                                                                                                                                                                                         (INSP ) INST PASTEUR.
(INRM ) INSERM INST NAT SANTE RE.
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Human immunodeficiency virus.
Simian immunodeficiency virus.
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                                                                                                      Simian immunodeficiency virus
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94.1%;
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                                                                                                                                                                                                 90EP-0401520
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(first entry)
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                                                                                        Human immunodeficiency
                                                                                                                                                                                                                                                                                                        Montagnier
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08-SEP-1998
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                                                                                                                                                                  19-DEC-1990
                                                                                                                                   EP403333-A.
                                                                                                                                                                                                                                                                                                        Moncany M,
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Best Local &
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AAT98040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                            Gaps
                                                                                                                                                                                                                                                                                                          CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8;
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                Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8
                                           Indels
                                                                                                                                                                                                                                                                           CD28 inhibiting phosphorothioate oligonucleotide RT09S.
              Score 16.4; DB 17;
Pred. No. 2e+03;
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                                  Mismatches
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94.48;
            Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                          phosphorothioate; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TAMR/) TAM R C.
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05-MAR-1991
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Tam RC;

Query Match

Best Loc Matches

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Gaps

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Shannon M;
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                                                                                                                                                                                              The oligonucleotides AAT98010-T98059 are useful as primers for nucleic acid amplification of conserved sequences of the gag, vpr, pol or vpu genes of the HIV-1 strains Bru, Mal, Eli, HIV-2 ROD or simian immunodeficiency virus (SIV) MAC or the nef2, vif2 or vpx genes of HIV-2 ROD and SIV MAC. This primer is targetted to sequences in the vpx gene of the viral strains. The sequences are therefore used to detect HIV-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene; Rho GTPase; signal transduction; gene expression; cancer; vaccine; gene therapy; transgenic; ss.
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                               Oligo-nucleotide primers for amplifying retroviral nucleic acids - comprising conserved sequences of human immunodeficiency virus and simian immunodeficiency virus genes
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Pred. No. 4.5e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human POSHL1 scanning oligonucleotide SEQ ID NO 1934.
                                                  (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
(INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                     the viral strains. The sequences are therefor HIV-2 or SIV infections. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                            Sequence 21 BP; 5 A; 2 C; 13 G; 1 T; 0 other;
                                                                                                                                                                         Claim 10; Page 21; 23pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABV91221 standard; DNA; 17 BP.
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2001WO-US00667.
2001WO-US00668.
2001WO-US00669.
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2001WO-US00664.
2001WO-US00665.
         89FR-0007354.
89FR-0012371.
90EP-0401520.
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Best Local Similarity 94.1%;
Matches 16; Conservative
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2001US-0328205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JAN-2002; 2002EP-0001165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                     Moncany M, Montagnier L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AEOM-) AEOMICA INC
                                                                                                          WPI; 1997-538622/50.
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30-JAN-2001; 2
30-JAN-2001; 2
30-JAN-2001; 2
30-JAN-2001; 2
30-JAN-2001; 2
                     20-SEP-1989;
05-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP1239051-A2
          02-JUN-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABV91221;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ABV91221/c
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The invention relates to an isolated SH3 domain (POSH)-like signalling protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino acids (SI, ABB83999), a sequence having 65% sequence identity to (SI), (C) acids (SI, ABB83999), a sequence having 65% sequence identity to (SI), acids (SI) having 95% deviations, especially conservative substitutions or a fragment of the sequences comprising at least 8 contiguous amino acids. (C) adaptor protein that interacts with Rho family small GTPases as well as adaptor protein that interacts with Rho family small GTPases as well as downstream components of the signal transduction pathway. (I) is useful contident of acids (II) and nucleic acids (II) caused by altered expression of human POSHL1 including disease and treating caused by altered expression of human POSHL1 including disease and (II) is useful in gene therapy. (II) is useful for constructing microarrays which are useful for measuring and for surveying gene expression and creating transgenic non-human animals capable of producing the proteins. The present sequence is that of a scanning oligonucleotide useful in examples of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The present sequence did not form part of the printed specification, but is based on sequence information supplied to Derwent by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, POSHL 1, SH3 domain, POSH-like signalling protein 1, oncogene, Rho GTPase, signal transduction, gene expression, cancer, vaccine, gene therapy, transgenic, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                           Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL-1, useful for treating disorders associated with decreased expression or activity of human POSHL1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                   Example 2; SEQ ID NO 1934; 60pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.3%; Score 15; DB 24; Length 17;
100.0%; Pred. No. 6.5e+03;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human POSHL1 scanning oligonucleotide SEQ ID NO 1935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 17 BP; 1 A; 12 C; 0 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
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30-JAN-2001; 2001WO-US00665.
30-JAN-2001; 2001WO-US00666.
30-JAN-2001; 2001WO-US00667.
30-JAN-2001; 2001WO-US00668.
30-JAN-2001; 2001WO-US00669.
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Best Local Similarity luv...
Las 15; Conservative
WPI; 2002-684061/74.
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Rho GTPase, signal transduction, gene expression, cancer, vaccine,
gene therapy, transgenic, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                  Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL-1, useful for treating disorders associated with decreased expression or activity of human POSHL1 -
                                                                                                                                                                                                                                                                        English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human POSHL1 scanning oligonucleotide SEQ ID NO 1936.
                                                                                                                                                                                                                                                                        Example 2; SEQ 1D NO 1935; 60pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15; DB 24; L
Pred. No. 6.5e+03;
0; Mismatches 0;
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100.0%; Pre
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30-JAN-2001; 2001WO-US00664.
30-JAN-2001; 2001WO-US00665.
30-JAN-2001; 2001WO-US00666.
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23-MAY-2001; 2001US-0864761.
10-OCT-2001; 2001US-0328205.
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                                                                                                                                                WPI; 2002-684061/74.
                                                               (AEOM-) AEOMICA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
es 15; Conserv
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                                                                                                       Shannon M;
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Matches
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ID ABV9
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The invention relates to an isolated SH3 domain (POSH)-like signalling protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino cids (SI) ABB83999), a sequence having 65% sequence identity to (SI), configurations, especially conservative substitutions or a fragment of the sequences comprising at least 8 contiguous amino acids. CC fragment of the sequences comprising at least 8 contiguous amino acids. CC daptor protein that interacts with Rho family small GTPases as well as downstream components of the signal transduction pathway. (I) is useful contidentifying a specific binding partner. (I) and nucleic acids (II) caused by altered expression of human POSHL including disease and treating cancer, they useful in the development of vaccines and (II) is useful in gene therapy. (II) is useful for constructing microarrays which creating transgenic non-human animals capable of producing the proteins. The present sequence is that of a scanning oligonucleotide useful in examples of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The present sequence did not form part of the printed specification, but is based on sequence information supplied to Derwent by the European Patent Office.
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                                                                                                                                                                                                                                                                                                                                                                      Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL-1, useful for treating disorders associated with decreased expression or activity of human POSHL1 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 83.3%; Score 15; DB 24; L Local Similarity 100.0%; Pred. No. 6.5e+03; es 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 1 A; 12 C; 1 G; 3 T; 0 other;
30-JAN-2001; 2001WO-US00667.
30-JAN-2001; 2001WO-US00668.
30-JAN-2001; 2001WO-US00669.
30-JAN-2001; 2001WO-US00670.
23-MAY-2001; 2001US-0864761.
10-OCT-2001; 2001US-0328205.
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15-APR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                    WPI; 2002-684061/74.
                                                                                                                                                                                                     (AEOM-) AEOMICA INC
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                                                                                                                                                                                                                                                                Shannon M;
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Treatment of immune system-mediated diseases by inhibiting expression of CD28, IL-2, gamma-interferon or IL-8

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                                                                                                                                                                                The present oligonuclectide reduces T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc.. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8;
                                                                                                                               Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD28 inhibiting phosphorothioate oligonucleotide RT03S
                                                                                                                                                                                                                                                                                  Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
                                                                                                                                                                  Claim 9; Page 54; 77pp; English.
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                                 95US-0387041.
95US-0529878.
95US-0387041.
95US-0529878.
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                  96WO-US01507
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                                                                                                                                                                                                                                                                                                            Similarity 88.9
16; Conservative
                                                                             (ICNC ) ICN PHARM INC
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                                                                                                                WPI; 1996-384228/38.
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                                 09-FEB-1995;
18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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                  05-FEB-1996;
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Matches 16;
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15-AUG-1996
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The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated
                                        The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothioate oligonucleotide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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88.9%; Pred. No. 7.6e+03;
live 0; Mismatches 2;
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Pred. No. 7.6e+03;
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Example; Column 21; 45pp; English
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                                                                                                                                                     present invention.
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G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection; antigen presenting cell activation; natural killer cell; septic shock; cytotoxic T-lymphocyte; inflammation; autoimmune disease; rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis; Kawasaki syndrome; graft-versus-host disease; transplant rejection; helper T cell response 1-mediated disease; Lyme arthritis; Streptococcal induced arthritis; chronic inflammatory bowel disease; psoriasis vulgaris; experimental allergic encephalomyelitis; insulin-dependent diabetes mellitus; bacterial infection; tumour; ss. parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Compositions comprising G-motif oligonucleotides useful for treating e.g. septic shock, rheumatoid arthritis, diabetes and human immunodeficiency virus infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide seguence of G-motif oligonucleotide GR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heeg K;
99WO-EP06502
                                                                                                                                                                                                                               AAZ99625 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                         12-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wagner H, Lipford GB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-256970/22.
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The present sequence represents a G-motif oligonucleotide of the invention. The specification describes compositions comprising G-motif coligonucleotides inhibit activation of antigen presenting cells by inhibiting the uptake of DNA by a cell, by stimulating natural killer cells, or by co-stimulating cytotoxic

T-lymphocytes. The G-motif oligonucleotides may be used for the productions of vaccines for treating septic shock, inflammation, autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease, carcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host disease and transplant rejection), helper T cell Lyme arthritis, chronic inflammatory bowel disease, psoriasis vulgaris, experimental allergic encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis), viral infections (e.g. Cytomegalovirus and tumnours. They may also be used to induce proliferation of bone marrow cells, especially macrophage precursor cells.

Seguence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;

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0
                            Gaps
                            .,
   Length 18;
                          Indels
Score 14.8; DB 21;
Pred. No. 7.6e+03;
0; Mismatches 2;
 Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
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18
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G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection; antigen presenting cell activation; natural killer cell; septic shock; cytotoxic T-lymphocyte; inflammation; autoimmune disease; rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis; Kawasaki syndrome; graft-versus-host disease; transplant rejection; helper T cell response 1-mediated disease; Lyme arthritis; streptococcal induced arthritis; chronic inflammatory bowel disease; psoriasis vulgaris; experimental allergic encephalomyelitis; insulin-dependent diabetes mellitus; bacterial infection; tumour; ss. parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.
                                                             Nucleotide sequence of non-G-motif oligonucleotide GRF1comp.
AAZ99650 standard; DNA; 18 BP
                                          12-JUL-2000 (first entry)
                    AAZ99650;
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(CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH. 99WO-EP06502. 98EP-0116652. 03-SEP-1999; 03-SEP-1998;

WO200014217-A2

Synthetic.

16-MAR-2000.

Heeg K; Wagner H, Lipford GB, WPI; 2000-256970/22. Compositions comprising G-motif oligonucleotides useful for e.g. septic shock, rheumatoid arthritis, diabetes and human immunodeficiency virus infections -

Example 14; Page 32; 75pp; English.

The present sequence represents a non-G-motif oligonucleotide of the invention. The specification describes compositions comprising G-motif oligonucleotides inhibit activation of antigen presenting cells by inhibiting the uptake of DNA by a cell, by stimulating natural killer cells, or by co-stimulating cytotoxic corproductions of vaccines for treating septic shock, inflammation, autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease, corproductions of vaccines for treating septic shock, inflammation, autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease, corproductions, multiple sclerosis, Kawasaki syndrome, graft-versus-host diseases (e.g. Streptococcal induced arthritis, Lymme arthritis, chronic concephalomyelitis, and insulin-dependent diabetes mellitus), bacterial infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis), viral infections (e.g. Cytomegalovirus and human immunodeficiency virus (HIV)-infections), spontaneous abortions and tumours. They may also be used to induce proliferation of bone marrow cells, especially macrophage procursor cells.

Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;

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Gaps
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       Length 18;
                             Indels
82.2%; Score 14.8; DB 21;
88.9%; Pred. No. 7.6e+03;
                  Local Similarity 88.9
nes 16; Conservative
          Query Match
                              Matches
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us-09-331-204a-7.szlm22.rng

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Reduction, T cell, CD28; gene expression; treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; psoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR; systemic lupus erythematosus; inflammatory bowel disease; triplex forming; oligonucleotide; 5'-untranslated region; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present oligonucleotide reduces T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple solerosis, uveitis, rheumatoid disease, etc. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release.
(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligo:nucleotide which reduces CD28 gene expression in T cells for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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                                                                                                                                                                                              Triplex forming oligo targetting CD28 5'-UTR (nt 58-78).
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18 TTGGAGGGGTGGTGGGG 1
                                                                                         AAT36197 standard; DNA; 21 BP.
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95US-0529878.
95US-0387041.
95US-0529878.
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Best Local Similarity 88.9%;
Matches 16; Conservative
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18-SEP-1995;
09-FEB-1995;
18-SEP-1995;
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15-APR-1997
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October 27, 2003, 10:32:29 ; Search time 376.114 Seconds (without alignments) 1957.844 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                              2888711 seqs, 20454813386 residues
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Maximum Match 100%
Listing first 45 summaries
                                      OM nucleic - nucleic search, using sw model
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AX023402 Sequence AX023427 Sequence	AX418779 Sequence A31974 Synthetic H	AR131393 Sequence BD001798 Immunogen	AX532425 Sequence	AX532427 Sequence	AX477615 Sequence AX505035 Sequence	128584 Sequence 37	158/46 Sequence 3/ AR297674 Sequence	AX662935 Sequence	AK029938 Sequence AX214603 Sequence	AX215452 Sequence	AROSS448 Sequence AX600765 Sequence	E04543 linker. 9/1	Akzizy/j Sequence AX418780 Sequence	BD177744 A method	AR061827 Sequence AR252818 Sequence	AX532424 Sequence	AX532428 Sequence ax188499 Sequence	AX235037 Sequence	AX532447 Sequence	August Nucleoride A04686 Nucleotide	AR012711 Sequence	ARU3665/ Sequence AR088921 Sequence	AR152368 Sequence	AR012712 Sequence	ARU36658 Seguence ABORA622 Seguence	AR152369 Sequence	AR232303 Sequence	AA488033 Sequence BD138339 Antisense	AX023422 Sequence			linear PAT 15-SEP-2000					; WAGNER HERMANN (DE) ;
SUMMARIES	AX023402 AX023427	Pa.	~ ~	AX532425 AX532425				•		AKU29938 AX214603			E04543	AK212973 AX418780	BD177744	AR061827 AR252818	AX532424	AX532428 AX188499	AX235037	AX532447	A04686		00		-4.0	^ ^	1 10	~	AX488033 BD138339	- 01	ALIGNMENTS		18 bp DNA ent WO0014217.	802			K. and Wagner, H. tides and uses thereof A 17 16-MAR-2000;	, HEEG KLAUS (DE)
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PAT 08-JUL-1996

BASE COUNT ORIGIN

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FEATURES

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Unknown.
Unclassified.

1 (bases 1 to 21)

Moncany, M. and Montagnier, L.

Moncany, M. and Montagnier, L.

Nucleotide sequences derived from the genome of retroviruses of the HV-1, HV-2, and SIV type, and their uses in particular for the amplification of the genomes of these retroviruses and for the in vitro diagnosis of the diseases due to these viruses

Patent: US 6194142-A 45 27-FEB-2001;
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1 (bases 1 to 21)
Moncany, M. and Montagnier, L.
Nucleotide sequences of retroviral genomes of types HIV-I, HIV-2 and SIV, their uses for the amplification of these genomes and diagnosis in vitro of these viral infections Patent: EP 0403333-A 29 19-DEC-1990;
INSTITUT PASTEUR; INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
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/db_xref="taxon:32630"
/note="Antisense Oligonucleotide"
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                                                                         Score 13.8; DB 6;
Pred. No. 2.6e+05;
0; Mismatches 2;
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88.2%; Pred. No. 2.6e+05;
live 0; Mismatches 2;
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Sequence 45 from patent US 6194142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lipford,G.B., Heeg,K. and Wagner,H.
G-motif Oligonucleotides and uses thereof
Patent: WO 0014217-A 42 16-MAR-2000;
LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ; WAGNER HERMANN (DE)
CPG IMMUNOPHARMACEUTICALS GMBH (DE)
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/organism="synthetic construct"

/mol type="genomic DNA"

/db xref="taxon:32630"

/note="synthetic, no natural origin"

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larity 94.4%; Pred. No. 2.4e+04;
Conservative 0; Mismatches 1;
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Pred. No. 2.4e+04;
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Antisense modulation of ptp1b expression
Patent: WO 0210378-A 174 07-FEB-2002;
ISIS PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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/organism="synthetic construct"
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AX418779
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Sequence 42 from Patent WO0014217.
AX023427
AX023427.1 GI:10183827
 CPG IMMUNOPHARMACEUTICALS GMBH (DE)
Location/Qualifiers
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synthetic construct
artificial sequences.
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Best Local Similarity 94.4%;
Matches 17; Conservative
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Matches 17; Conserv
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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

FEATURES

BASE COUNT ORIGIN

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ORGANISM

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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 4e+05;
0; Mismatches 1;
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Patent: EP 1239051-A 1935 11-SEP-2002;
Aeomica, Inc. (US)
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Patent: BP 1239051-A 1936 11-SEP-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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AX532427
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Seguence 1935 from Patent EP1239051.
AX532426
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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93.3%;
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AX532427/c
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BD001798.1 GI:18626357
JP 2000093187-A/45.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 21)
Moncany, M. and Montagnier, L.
Immunogenic compounds containing a translation product of
                                                                                                                                                                                                                       BD001798

Immunogenic compounds containing a translation product of nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and SIV
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/organism='Artificial Sequence'
Location/Qualifiers
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 Pred. No. 2.6e+05;
); Mismatches 2; Indels
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
a 2 c 13 g 1 t
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Pred. No. 2.6e+05;
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Patent: EP 1239051-A 1934 11-SEP-2002;
Aeomica, Inc. (US)
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Sequence 1934 from Patent BP1239051.
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Best Local Similarity 88.2%; Pr
Matches 15; Conservative 0;
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AX532425.1 GI:25256625
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Homo sapiens
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Best Local Similarity 88.2
Matches 15, Conservative
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PAT 07-0CT-1997
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US 6537751.
                                                                    DNA
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Watanabe, K.A., Ren, W.-Y. and Weil, R.
Complementary DNA and toxins
Patent: US 5652350-A 37 29-JUL-1997;
Location/Qualifiers
                                                                                                                                                                              1 (bases 1 to 19)
Watanabe, K.A., Ren, W.-Y. and Weil, R.
Complementary DNA and toxins
Patent: US 5571937-A 37 05-NOV-1996;
Location/Qualifiers
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Sequence 37 from patent US 5652350.
IS8746
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Sequence 37 from patent US 5571937.
128584
128584.1 GI:1819360
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Sequence 9409 from patent
AR297674
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AR297674/c
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Length 17;
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Pred. No. 3.9e+05;
0; Mismatches 1; Indels
Score 13.4; DB 6; Length 1
Pred. No. 4e+05;
0; Mismatches 1; Indels
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Thf-inducible promoters and methods for using Patent: WO 0246433-A 67 13-JUN-2002;
Saus, Juan (ES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.4%; Score 13.4; DB 6;
93.3%; Pred. No. 3.9e+05;
iive 0; Mismatches 1;
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/organism="synthetic construct"
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Primer ON-DHFR-F1"
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Patent: WO 0246378-A 67 13-JUN-2002;
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Sequence 67 from Patent WO0246433.
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Sequence 67 from Patent WO0246378.
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/organism="Homo sapiens"
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/note="Antisense PCR primer for CC3 promoter (spec Table IIIa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Poole, J., Roninson, I.B. and Chang, B.D.
Reagents and methods for identifying and modulating expression of genes regulated by cdk inhibitors
Patent: WO 02066681-A 22 29-AUG-2002;
THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ILLINOIS (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
Patent: US 6537751-A 9409 25-MAR-2003;
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Pred. No. 3.8e+05;
0; Mismatches 1; Indels
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/organism="unknown"
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